

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:25:17 ; Search time 6778 Seconds
(without alignments)
13028.785 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccggggcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | 8 | | Query | | DB | ID | Description |
|---------------|--------|-------|--------|---|----------|--------------------|-------------|
| | Score | Match | Length | | | | |
| 1 | 1180.4 | 50.9 | 1182 | 9 | AY404343 | AY404343 Homo sapi | |
| 2 | 912.2 | 39.3 | 2197 | 3 | AK050128 | AK050128 Mus muscu | |
| 3 | 857.4 | 37.0 | 1180 | 9 | AY404344 | AY404344 Pan trogl | |
| 4 | 853.2 | 36.8 | 879 | 5 | BQ216829 | BQ216829 AGENCOURT | |
| 5 | 754 | 32.5 | 759 | 7 | CN396938 | CN396938 170004177 | |
| 6 | 738 | 31.8 | 916 | 6 | CD050395 | CD050395 AGENCOURT | |
| 7 | 733.8 | 31.6 | 1185 | 9 | AY404345 | AY404345 Mus muscu | |
| 8 | 731.6 | 31.5 | 1353 | 3 | AK041045 | AK041045 Mus muscu | |

| | | | | | | | | |
|---|----|-------|------|------|---|----------|----------|-------------|
| | 9 | 522.4 | 22.5 | 978 | 4 | BI102968 | BI102968 | 602888578 |
| | 10 | 506.4 | 21.8 | 510 | 7 | CN396939 | CN396939 | 170005999 |
| | 11 | 490.6 | 21.1 | 717 | 7 | CR769328 | CR769328 | DKFZp4690 |
| | 12 | 488.6 | 21.1 | 761 | 4 | BI559553 | BI559553 | 603252894 |
| c | 13 | 463.6 | 20.0 | 694 | 2 | AW173071 | AW173071 | xj82g11.x |
| c | 14 | 457.6 | 19.7 | 659 | 6 | CB435346 | CB435346 | 615435 MA |
| | 15 | 452.6 | 19.5 | 1723 | 3 | AK052644 | AK052644 | Mus muscu |
| | 16 | 452.2 | 19.5 | 771 | 7 | CR767782 | CR767782 | DKFZp469C |
| | 17 | 450 | 19.4 | 724 | 6 | CB952493 | CB952493 | AGENCOURT |
| | 18 | 444.4 | 19.2 | 481 | 6 | CB158774 | CB158774 | K-EST0218 |
| c | 19 | 442 | 19.1 | 583 | 1 | AI694348 | AI694348 | wd45g04.x |
| c | 20 | 437.8 | 18.9 | 462 | 5 | BX109306 | BX109306 | BX109306 |
| c | 21 | 435.8 | 18.8 | 439 | 1 | AA633698 | AA633698 | ag87a11.s |
| | 22 | 431.6 | 18.6 | 899 | 4 | BI246549 | BI246549 | 602958449 |
| c | 23 | 430 | 18.5 | 430 | 1 | AI917116 | AI917116 | ts52a02.x |
| c | 24 | 422 | 18.2 | 422 | 1 | AI580389 | AI580389 | tm42f08.x |
| c | 25 | 417 | 18.0 | 1055 | 1 | AI654867 | AI654867 | wb65c12.x |
| | 26 | 415.8 | 17.9 | 660 | 2 | BB221592 | BB221592 | BB221592 |
| c | 27 | 410.2 | 17.7 | 478 | 1 | AI015041 | AI015041 | ov51a05.s |
| | 28 | 407.8 | 17.6 | 585 | 7 | CR770709 | CR770709 | DKFZp469J |
| | 29 | 406.4 | 17.5 | 901 | 4 | BI827790 | BI827790 | 603075472 |
| | 30 | 404.8 | 17.4 | 1021 | 7 | CK231266 | CK231266 | ILLUMIGEN |
| c | 31 | 400 | 17.2 | 543 | 2 | AW236852 | AW236852 | xm49h11.x |
| | 32 | 398.4 | 17.2 | 552 | 7 | CV029784 | CV029784 | 8702 Full |
| | 33 | 396.4 | 17.1 | 721 | 4 | BG972539 | BG972539 | 602841125 |
| c | 34 | 393.4 | 17.0 | 470 | 1 | AA974327 | AA974327 | oq10g06.s |
| | 35 | 389 | 16.8 | 531 | 8 | AQ386013 | AQ386013 | RPCI11-14 |
| c | 36 | 388.6 | 16.8 | 449 | 1 | AI217703 | AI217703 | qh15e09.x |
| | 37 | 387.8 | 16.7 | 738 | 6 | CB954127 | CB954127 | AGENCOURT |
| | 38 | 386.6 | 16.7 | 751 | 8 | AQ748070 | AQ748070 | HS_5538_A |
| | 39 | 384.8 | 16.6 | 886 | 4 | BI101074 | BI101074 | 602886333 |
| c | 40 | 384.6 | 16.6 | 454 | 1 | AA970255 | AA970255 | op64h06.s |
| | 41 | 384.4 | 16.6 | 751 | 6 | CB952810 | CB952810 | AGENCOURT |
| | 42 | 384.2 | 16.6 | 582 | 5 | BP274546 | BP274546 | BP274546 |
| | 43 | 380.8 | 16.4 | 578 | 5 | BP275078 | BP275078 | BP275078 |
| c | 44 | 380.4 | 16.4 | 580 | 6 | CB423692 | CB423692 | 597208 MA |
| c | 45 | 376.8 | 16.2 | 566 | 6 | CB433850 | CB433850 | 610302 MA |
| | 46 | 375 | 16.2 | 460 | 7 | R19994 | R19994 | yg38h02.r1 |
| | 47 | 374.2 | 16.1 | 759 | 4 | BG971626 | BG971626 | 602840706 |
| | 48 | 372.4 | 16.1 | 565 | 4 | BI538734 | BI538734 | 434264 MA |
| | 49 | 370.4 | 16.0 | 910 | 4 | BI099853 | BI099853 | 602884666 |
| | 50 | 368.4 | 15.9 | 763 | 6 | CD241803 | CD241803 | AGENCOURT |
| | 51 | 365.4 | 15.8 | 419 | 7 | CR740722 | CR740722 | CR740722 |
| c | 52 | 364.6 | 15.7 | 619 | 9 | CE584093 | CE584093 | tigr-gss- |
| | 53 | 361.6 | 15.6 | 1193 | 4 | BI102573 | BI102573 | 602889579 |
| c | 54 | 357 | 15.4 | 363 | 7 | Z39483 | Z39483 | HSC1BC022 n |
| | 55 | 354.4 | 15.3 | 360 | 5 | BP431975 | BP431975 | BP431975 |
| c | 56 | 346.8 | 14.9 | 357 | 1 | AA747964 | AA747964 | nx79a08.s |
| | 57 | 341 | 14.7 | 880 | 4 | BI143297 | BI143297 | 602907843 |
| | 58 | 339.2 | 14.6 | 1082 | 3 | BC024453 | BC024453 | Mus muscu |
| c | 59 | 336.2 | 14.5 | 363 | 2 | BF510946 | BF510946 | UI-H-BI4- |
| | 60 | 335 | 14.4 | 908 | 2 | BF788011 | BF788011 | 602113215 |
| | 61 | 334.4 | 14.4 | 342 | 5 | BP431877 | BP431877 | BP431877 |
| | 62 | 331.8 | 14.3 | 349 | 7 | F06529 | F06529 | HSC1BC021 n |
| | 63 | 330.2 | 14.2 | 538 | 4 | BG971731 | BG971731 | 602838268 |
| | 64 | 329.6 | 14.2 | 776 | 4 | BI220321 | BI220321 | 602935611 |
| | 65 | 329 | 14.2 | 956 | 2 | BF784727 | BF784727 | 602111365 |

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|---|-----|-------|------|------|---|----------|----------|-----------|
| | 66 | 323 | 13.9 | 785 | 2 | BF780827 | BF780827 | 602105713 |
| c | 67 | 317 | 13.7 | 706 | 9 | CE140389 | CE140389 | tigr-gss- |
| | 68 | 314.8 | 13.6 | 772 | 4 | BI099719 | BI099719 | 602884581 |
| | 69 | 314.6 | 13.6 | 769 | 2 | AW044731 | AW044731 | uml3h02.y |
| c | 70 | 314.4 | 13.6 | 436 | 8 | AQ476159 | AQ476159 | CITBI-E1- |
| | 71 | 308.4 | 13.3 | 875 | 2 | BF788790 | BF788790 | 602107191 |
| | 72 | 305.6 | 13.2 | 786 | 6 | CB953250 | CB953250 | AGENCOURT |
| | 73 | 304.2 | 13.1 | 890 | 4 | BI101705 | BI101705 | 602887533 |
| c | 74 | 303 | 13.1 | 799 | 7 | CK848020 | CK848020 | 970722 MA |
| | 75 | 301.2 | 13.0 | 777 | 4 | BG972946 | BG972946 | 602840675 |
| | 76 | 298.6 | 12.9 | 711 | 2 | BF785562 | BF785562 | 602112344 |
| | 77 | 298.6 | 12.9 | 965 | 2 | BF789220 | BF789220 | 602105115 |
| | 78 | 298.4 | 12.9 | 755 | 4 | BI220886 | BI220886 | 602937437 |
| | 79 | 296.4 | 12.8 | 878 | 2 | BF782452 | BF782452 | 602106160 |
| c | 80 | 296 | 12.8 | 455 | 2 | AW380602 | AW380602 | RC2-HT027 |
| | 81 | 294.6 | 12.7 | 453 | 1 | AA245657 | AA245657 | mx03a05.r |
| | 82 | 293.4 | 12.6 | 459 | 5 | BX951484 | BX951484 | DKFZp781F |
| | 83 | 293 | 12.6 | 913 | 4 | BG972966 | BG972966 | 602840774 |
| | 84 | 292.2 | 12.6 | 1452 | 2 | BF782437 | BF782437 | 602106145 |
| c | 85 | 290.2 | 12.5 | 429 | 2 | AW236558 | AW236558 | xm47g07.x |
| | 86 | 288.6 | 12.4 | 776 | 2 | BF781397 | BF781397 | 602104580 |
| | 87 | 288.2 | 12.4 | 713 | 4 | BI327590 | BI327590 | 602979770 |
| | 88 | 286.4 | 12.3 | 555 | 5 | BP332215 | BP332215 | BP332215 |
| | 89 | 284 | 12.2 | 551 | 2 | BF785590 | BF785590 | 602112377 |
| | 90 | 282.2 | 12.2 | 488 | 6 | CB433209 | CB433209 | 609534 MA |
| | 91 | 277.8 | 12.0 | 788 | 2 | BF781367 | BF781367 | 602104549 |
| | 92 | 277.6 | 12.0 | 863 | 7 | CF218052 | CF218052 | AGENCOURT |
| | 93 | 275.6 | 11.9 | 699 | 2 | AW319008 | AW319008 | un10f04.y |
| | 94 | 275.2 | 11.9 | 735 | 4 | BI332326 | BI332326 | 602983510 |
| | 95 | 273.4 | 11.8 | 371 | 2 | BE843851 | BE843851 | RC0-TN007 |
| | 96 | 273.2 | 11.8 | 696 | 2 | BB653699 | BB653699 | BB653699 |
| | 97 | 271.8 | 11.7 | 766 | 6 | CB600123 | CB600123 | AGENCOURT |
| | 98 | 271 | 11.7 | 904 | 2 | BF780781 | BF780781 | 602103058 |
| | 99 | 270.4 | 11.7 | 654 | 2 | AW318818 | AW318818 | un07h11.y |
| | 100 | 268 | 11.6 | 695 | 2 | BB598307 | BB598307 | BB598307 |
| | 101 | 267.8 | 11.5 | 1027 | 4 | BG969791 | BG969791 | 602838703 |
| | 102 | 267.4 | 11.5 | 668 | 2 | BB660895 | BB660895 | BB660895 |
| | 103 | 266.6 | 11.5 | 758 | 4 | BI332502 | BI332502 | 602981312 |
| | 104 | 264.4 | 11.4 | 782 | 4 | BG972529 | BG972529 | 602841114 |
| | 105 | 261.8 | 11.3 | 602 | 6 | CB601068 | CB601068 | AGENCOURT |
| | 106 | 261.6 | 11.3 | 380 | 7 | CR746104 | CR746104 | CR746104 |
| | 107 | 259.8 | 11.2 | 701 | 2 | BF787378 | BF787378 | 602113777 |
| | 108 | 258.8 | 11.2 | 812 | 4 | BG969879 | BG969879 | 602838824 |
| | 109 | 255.2 | 11.0 | 399 | 1 | AA245658 | AA245658 | mx03a06.r |
| c | 110 | 254.6 | 11.0 | 328 | 1 | AI671780 | AI671780 | wa05h05.x |
| c | 111 | 254.6 | 11.0 | 331 | 1 | AI613123 | AI613123 | ty71h04.x |
| c | 112 | 254.6 | 11.0 | 332 | 1 | AI672388 | AI672388 | ty64f01.x |
| | 113 | 254 | 10.9 | 916 | 2 | BF687218 | BF687218 | 602102243 |
| c | 114 | 253 | 10.9 | 923 | 5 | BX694171 | BX694171 | BX694171 |
| c | 115 | 252.6 | 10.9 | 920 | 5 | BX701766 | BX701766 | BX701766 |
| c | 116 | 251.4 | 10.8 | 922 | 5 | BX701212 | BX701212 | BX701212 |
| | 117 | 247.8 | 10.7 | 647 | 2 | BB637357 | BB637357 | BB637357 |
| c | 118 | 247.8 | 10.7 | 922 | 5 | BX686029 | BX686029 | BX686029 |
| | 119 | 246.8 | 10.6 | 581 | 1 | AI528034 | AI528034 | uj39b11.y |
| | 120 | 246.8 | 10.6 | 593 | 1 | AI526529 | AI526529 | uj39e10.y |
| c | 121 | 246.6 | 10.6 | 345 | 2 | AW779709 | AW779709 | hn84f05.x |
| | 122 | 246.6 | 10.6 | 383 | 5 | BX955526 | BX955526 | DKFZp781A |

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|-------|-------|------|------|---|----------|----------|-----------|
| 123 | 246.2 | 10.6 | 878 | 4 | BG973007 | BG973007 | 602841631 |
| 124 | 244.2 | 10.5 | 473 | 2 | BF659710 | BF659710 | maa23c04. |
| c 125 | 243.8 | 10.5 | 919 | 5 | BX698025 | BX698025 | BX698025 |
| 126 | 239.4 | 10.3 | 651 | 1 | AI527981 | AI527981 | uj38e11.y |
| 127 | 236.8 | 10.2 | 551 | 1 | AI876961 | AI876961 | uj36h03.y |
| 128 | 236.4 | 10.2 | 550 | 1 | AI526647 | AI526647 | uj41b09.y |
| 129 | 236 | 10.2 | 581 | 7 | CF171593 | CF171593 | B0844F01- |
| 130 | 235.4 | 10.1 | 726 | 6 | CB600351 | CB600351 | AGENCOURT |
| 131 | 233 | 10.0 | 534 | 1 | AI787373 | AI787373 | uj31b07.y |
| c 132 | 231.2 | 10.0 | 891 | 5 | BX687753 | BX687753 | BX687753 |
| c 133 | 230.8 | 9.9 | 347 | 1 | AI767712 | AI767712 | wh38h05.x |
| 134 | 228.8 | 9.9 | 533 | 1 | AI875380 | AI875380 | uk31e01.y |
| 135 | 228.4 | 9.8 | 549 | 1 | AI050425 | AI050425 | uc86b01.y |
| c 136 | 227.2 | 9.8 | 288 | 2 | AW235540 | AW235540 | xn19d12.x |
| 137 | 227.2 | 9.8 | 867 | 2 | BF785547 | BF785547 | 602112327 |
| 138 | 226.8 | 9.8 | 469 | 2 | AW610950 | AW610950 | un74c08.y |
| 139 | 225.2 | 9.7 | 531 | 4 | BI463768 | BI463768 | 603203473 |
| c 140 | 225.2 | 9.7 | 891 | 5 | BX699365 | BX699365 | BX699365 |
| 141 | 224.8 | 9.7 | 925 | 2 | BF781667 | BF781667 | 602104385 |
| 142 | 222.6 | 9.6 | 887 | 2 | BF785369 | BF785369 | 602111710 |
| 143 | 222.4 | 9.6 | 562 | 1 | AI746748 | AI746748 | ul07a01.y |
| 144 | 222.2 | 9.6 | 536 | 1 | AI787361 | AI787361 | uj31a06.y |
| 145 | 220 | 9.5 | 524 | 1 | AI876741 | AI876741 | uj35c01.y |
| 146 | 218.6 | 9.4 | 536 | 2 | AW226792 | AW226792 | um62c04.y |
| 147 | 217.8 | 9.4 | 638 | 4 | BI100051 | BI100051 | 602885109 |
| 148 | 217.6 | 9.4 | 517 | 5 | BX512263 | BX512263 | BX512263 |
| 149 | 216.6 | 9.3 | 533 | 1 | AI747909 | AI747909 | ul03h02.y |
| 150 | 216.6 | 9.3 | 555 | 2 | AW107039 | AW107039 | ul92b06.y |
| 151 | 216.6 | 9.3 | 649 | 2 | BF788330 | BF788330 | 602114069 |
| c 152 | 216.4 | 9.3 | 291 | 1 | AI521956 | AI521956 | ti79e06.x |
| 153 | 215 | 9.3 | 407 | 6 | CB434861 | CB434861 | 611551 MA |
| 154 | 214 | 9.2 | 715 | 4 | BG971579 | BG971579 | 602840635 |
| c 155 | 213.8 | 9.2 | 813 | 5 | BX693887 | BX693887 | BX693887 |
| 156 | 213 | 9.2 | 546 | 2 | AW475287 | AW475287 | un63h08.y |
| c 157 | 212.2 | 9.1 | 793 | 7 | CF219588 | CF219588 | AGENCOURT |
| c 158 | 211.8 | 9.1 | 796 | 7 | CF218053 | CF218053 | AGENCOURT |
| 159 | 211.4 | 9.1 | 769 | 2 | BF782853 | BF782853 | 602107722 |
| 160 | 210.6 | 9.1 | 611 | 1 | AL794601 | AL794601 | AL794601 |
| 161 | 208.8 | 9.0 | 515 | 2 | BF532434 | BF532434 | 602074477 |
| 162 | 208.4 | 9.0 | 1349 | 2 | BF686940 | BF686940 | 602102714 |
| 163 | 207.8 | 9.0 | 968 | 2 | BF780880 | BF780880 | 602105777 |
| 164 | 206.8 | 8.9 | 931 | 7 | CF238676 | CF238676 | AGENCOURT |
| 165 | 204.6 | 8.8 | 661 | 6 | BY732658 | BY732658 | BY732658 |
| 166 | 202.4 | 8.7 | 489 | 5 | BX522348 | BX522348 | BX522348 |
| c 167 | 197 | 8.5 | 253 | 1 | AI373521 | AI373521 | qz46f08.x |
| c 168 | 197 | 8.5 | 253 | 1 | AI492912 | AI492912 | qz42f01.x |
| 169 | 191.6 | 8.3 | 833 | 2 | BF786313 | BF786313 | 602112827 |
| 170 | 191.4 | 8.2 | 508 | 1 | AL803540 | AL803540 | AL803540 |
| c 171 | 191.4 | 8.2 | 721 | 4 | BJ640903 | BJ640903 | BJ640903 |
| 172 | 187.6 | 8.1 | 958 | 2 | BF782294 | BF782294 | 602106080 |
| 173 | 187.2 | 8.1 | 488 | 2 | AW105948 | AW105948 | um20c05.y |
| 174 | 186.8 | 8.1 | 752 | 6 | CB601161 | CB601161 | AGENCOURT |
| 175 | 186 | 8.0 | 470 | 2 | AW319385 | AW319385 | un15f02.y |
| 176 | 184.6 | 8.0 | 1783 | 3 | CR636858 | CR636858 | Tetraodon |
| c 177 | 183.2 | 7.9 | 361 | 1 | AA730192 | AA730192 | nw41a02.s |
| 178 | 183.2 | 7.9 | 375 | 1 | AA715548 | AA715548 | nv53g11.r |
| 179 | 183 | 7.9 | 758 | 4 | BG969488 | BG969488 | 602837021 |

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|-------|-------|-----|------|---|----------|----------|-----------|
| 180 | 179.8 | 7.8 | 478 | 1 | AI874790 | AI874790 | ul28b05.y |
| 181 | 179.4 | 7.7 | 389 | 5 | BY105462 | BY105462 | BY105462 |
| 182 | 179 | 7.7 | 820 | 7 | CF222788 | CF222788 | AGENCOURT |
| c 183 | 177.8 | 7.7 | 676 | 4 | BJ641175 | BJ641175 | BJ641175 |
| c 184 | 173.4 | 7.5 | 606 | 9 | CE149561 | CE149561 | tigr-gss- |
| c 185 | 172.2 | 7.4 | 603 | 9 | CE843398 | CE843398 | tigr-gss- |
| c 186 | 171.8 | 7.4 | 599 | 1 | AA758115 | AA758115 | ah68d01.s |
| 187 | 168.8 | 7.3 | 420 | 2 | BB846612 | BB846612 | BB846612 |
| 188 | 168.8 | 7.3 | 831 | 7 | CF219551 | CF219551 | AGENCOURT |
| c 189 | 168.4 | 7.3 | 673 | 1 | AI746432 | AI746432 | ul07a01.x |
| 190 | 168.2 | 7.2 | 443 | 1 | AI182048 | AI182048 | ud73d07.y |
| 191 | 167.4 | 7.2 | 209 | 7 | CR746121 | CR746121 | CR746121 |
| 192 | 166.6 | 7.2 | 463 | 1 | AI931234 | AI931234 | ul58e10.y |
| c 193 | 164 | 7.1 | 791 | 7 | CF219552 | CF219552 | AGENCOURT |
| 194 | 163.6 | 7.1 | 882 | 7 | CF239400 | CF239400 | AGENCOURT |
| 195 | 159.6 | 6.9 | 706 | 7 | CN059643 | CN059643 | Salamande |
| c 196 | 159.2 | 6.9 | 301 | 1 | AI891486 | AI891486 | ul59b08.x |
| 197 | 158.6 | 6.8 | 896 | 6 | CA973829 | CA973829 | AGENCOURT |
| 198 | 158.4 | 6.8 | 542 | 4 | BI218377 | BI218377 | 602937760 |
| 199 | 158.4 | 6.8 | 594 | 8 | AZ519016 | AZ519016 | RPCI-11-6 |
| 200 | 156.8 | 6.8 | 464 | 8 | AQ199079 | AQ199079 | RPCI11-67 |
| 201 | 156.2 | 6.7 | 771 | 7 | CF222154 | CF222154 | AGENCOURT |
| 202 | 155.8 | 6.7 | 426 | 1 | AI529289 | AI529289 | ui61f12.y |
| 203 | 153 | 6.6 | 434 | 2 | BB847184 | BB847184 | BB847184 |
| 204 | 152.4 | 6.6 | 428 | 2 | BB847987 | BB847987 | BB847987 |
| 205 | 151.6 | 6.5 | 936 | 6 | CA980884 | CA980884 | AGENCOURT |
| 206 | 151.4 | 6.5 | 387 | 1 | AA105944 | AA105944 | ml80g04.r |
| 207 | 151 | 6.5 | 1946 | 3 | AK050435 | AK050435 | Mus muscu |
| c 208 | 150 | 6.5 | 607 | 4 | BJ631992 | BJ631992 | BJ631992 |
| 209 | 149.4 | 6.4 | 2573 | 3 | AK004971 | AK004971 | Mus muscu |
| 210 | 148.2 | 6.4 | 438 | 2 | BB848332 | BB848332 | BB848332 |
| 211 | 147.8 | 6.4 | 1581 | 9 | AY418358 | AY418358 | Mus muscu |
| 212 | 147.6 | 6.4 | 426 | 2 | BB847742 | BB847742 | BB847742 |
| 213 | 147.6 | 6.4 | 858 | 7 | CN986339 | CN986339 | 61948_125 |
| c 214 | 147 | 6.3 | 651 | 5 | BQ388289 | BQ388289 | NISC_mn28 |
| 215 | 146.4 | 6.3 | 827 | 7 | CF219587 | CF219587 | AGENCOURT |
| 216 | 146.2 | 6.3 | 426 | 2 | BB846847 | BB846847 | BB846847 |
| 217 | 145.8 | 6.3 | 418 | 5 | BY006680 | BY006680 | BY006680 |
| 218 | 145.6 | 6.3 | 838 | 5 | BU899699 | BU899699 | AGENCOURT |
| 219 | 144.8 | 6.2 | 424 | 2 | BB848230 | BB848230 | BB848230 |
| 220 | 144.6 | 6.2 | 429 | 2 | BB847232 | BB847232 | BB847232 |
| 221 | 144.2 | 6.2 | 493 | 1 | AI746700 | AI746700 | ul06d06.y |
| c 222 | 144.2 | 6.2 | 644 | 4 | BJ098498 | BJ098498 | BJ098498 |
| 223 | 143.6 | 6.2 | 437 | 1 | AI891771 | AI891771 | ul59b08.y |
| c 224 | 143.4 | 6.2 | 1108 | 7 | CO645645 | CO645645 | ILLUMIGEN |
| 225 | 142 | 6.1 | 438 | 2 | BB847387 | BB847387 | BB847387 |
| 226 | 141.4 | 6.1 | 430 | 1 | AL778797 | AL778797 | AL778797 |
| 227 | 140.8 | 6.1 | 369 | 2 | BB843421 | BB843421 | BB843421 |
| 228 | 140.6 | 6.1 | 933 | 7 | CO775326 | CO775326 | ILLUMIGEN |
| 229 | 140.2 | 6.0 | 1896 | 3 | AK002736 | AK002736 | Mus muscu |
| 230 | 138.8 | 6.0 | 418 | 2 | BB847984 | BB847984 | BB847984 |
| 231 | 138.6 | 6.0 | 362 | 2 | BB847614 | BB847614 | BB847614 |
| 232 | 138.6 | 6.0 | 370 | 2 | BB843440 | BB843440 | BB843440 |
| 233 | 138.2 | 6.0 | 528 | 1 | AI876859 | AI876859 | uj35a11.y |
| 234 | 137.8 | 5.9 | 1892 | 3 | AK034801 | AK034801 | Mus muscu |
| 235 | 137.4 | 5.9 | 2575 | 3 | BC048920 | BC048920 | Mus muscu |
| 236 | 136 | 5.9 | 960 | 5 | BQ713091 | BQ713091 | AGENCOURT |

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|-------|-------|-----|------|---|-----------|----------|------------|
| 237 | 133.8 | 5.8 | 2895 | 3 | AK083294 | AK083294 | Mus muscu |
| 238 | 132.6 | 5.7 | 825 | 5 | BP443785 | BP443785 | BP443785 |
| 239 | 132 | 5.7 | 1118 | 7 | CK028589 | CK028589 | AGENCOURT |
| 240 | 131.6 | 5.7 | 1642 | 6 | CD013996 | CD013996 | 90117309 |
| 241 | 131.4 | 5.7 | 927 | 5 | BQ925596 | BQ925596 | AGENCOURT |
| 242 | 130.8 | 5.6 | 1004 | 5 | BQ942104 | BQ942104 | AGENCOURT |
| 243 | 130.4 | 5.6 | 718 | 4 | BJ038707 | BJ038707 | BJ038707 |
| 244 | 130.2 | 5.6 | 928 | 7 | CK871071 | CK871071 | AGENCOURT |
| 245 | 130 | 5.6 | 821 | 7 | CK953540 | CK953540 | 4093245 B |
| 246 | 129.8 | 5.6 | 420 | 5 | BY006031 | BY006031 | BY006031 |
| 247 | 129.8 | 5.6 | 432 | 2 | BB846687 | BB846687 | BB846687 |
| c 248 | 129.4 | 5.6 | 740 | 4 | BJ640531 | BJ640531 | BJ640531 |
| 249 | 129.2 | 5.6 | 424 | 2 | BB846725 | BB846725 | BB846725 |
| 250 | 129.2 | 5.6 | 599 | 4 | BI387131 | BI387131 | BFL26_001 |
| 251 | 129.2 | 5.6 | 631 | 4 | BI387132 | BI387132 | BFL26_001 |
| 252 | 129 | 5.6 | 818 | 2 | BF687167 | BF687167 | 602102982 |
| 253 | 128.2 | 5.5 | 1581 | 9 | AY418356 | AY418356 | Homo sapi |
| 254 | 127.4 | 5.5 | 425 | 2 | BB844689 | BB844689 | BB844689 |
| 255 | 127.2 | 5.5 | 383 | 5 | BY005749 | BY005749 | BY005749 |
| 256 | 127.2 | 5.5 | 415 | 2 | BB847175 | BB847175 | BB847175 |
| 257 | 124.8 | 5.4 | 430 | 5 | BY006688 | BY006688 | BY006688 |
| 258 | 124.8 | 5.4 | 1023 | 6 | CD013994 | CD013994 | 90130114 |
| 259 | 124.8 | 5.4 | 1336 | 6 | CD013995 | CD013995 | 90130122 |
| 260 | 124.6 | 5.4 | 735 | 7 | CK949530 | CK949530 | 4074896 B |
| 261 | 124 | 5.3 | 1783 | 3 | AK050327 | AK050327 | Mus muscu |
| 262 | 123.6 | 5.3 | 338 | 2 | BB846932 | BB846932 | BB846932 |
| 263 | 123 | 5.3 | 930 | 5 | BQ934372 | BQ934372 | AGENCOURT |
| 264 | 123 | 5.3 | 1957 | 3 | CR671108 | CR671108 | Tetraodon |
| 265 | 122.8 | 5.3 | 423 | 5 | BY006690 | BY006690 | BY006690 |
| 266 | 122.6 | 5.3 | 825 | 5 | BU240452 | BU240452 | 603323679 |
| 267 | 122.4 | 5.3 | 830 | 6 | CA493727 | CA493727 | AGENCOURT |
| 268 | 122 | 5.3 | 977 | 7 | CO579097 | CO579097 | ILLUMIGEN |
| c 269 | 121.6 | 5.2 | 527 | 8 | AQ993185 | AQ993185 | RPCI-23-3 |
| c 270 | 121.6 | 5.2 | 694 | 8 | AZ085726 | AZ085726 | RPCI-23-6 |
| 271 | 121.6 | 5.2 | 810 | 7 | CO574370 | CO574370 | AGENCOURT |
| 272 | 121.6 | 5.2 | 843 | 7 | CO558457 | CO558457 | AGENCOURT |
| c 273 | 121.2 | 5.2 | 567 | 4 | BI443347 | BI443347 | dai90a05. |
| 274 | 121 | 5.2 | 340 | 2 | BB846937 | BB846937 | BB846937 |
| c 275 | 120.8 | 5.2 | 405 | 1 | AI433413 | AI433413 | ti65c03.x |
| 276 | 120.8 | 5.2 | 2099 | 3 | AK008601 | AK008601 | Mus muscu |
| 277 | 120.4 | 5.2 | 596 | 1 | AL781524 | AL781524 | AL781524 |
| 278 | 120.4 | 5.2 | 651 | 1 | AA255327 | AA255327 | mz84f10.r |
| 279 | 119.8 | 5.2 | 1130 | 3 | CR646329 | CR646329 | Tetraodon |
| c 280 | 119.6 | 5.2 | 594 | 9 | FR0049565 | AL605374 | Fugu rubr |
| 281 | 119.2 | 5.1 | 737 | 7 | CO562727 | CO562727 | AGENCOURT |
| 282 | 119 | 5.1 | 795 | 5 | BX880311 | BX880311 | BX880311 |
| 283 | 119 | 5.1 | 835 | 7 | CO573273 | CO573273 | AGENCOURT |
| 284 | 119 | 5.1 | 882 | 4 | BI144244 | BI144244 | 602907984 |
| 285 | 118.8 | 5.1 | 494 | 1 | AI785732 | AI785732 | uj37h01.y |
| 286 | 118.8 | 5.1 | 629 | 5 | BP138260 | BP138260 | BP138260 |
| c 287 | 118 | 5.1 | 148 | 2 | BF089587 | BF089587 | CM2-HT094 |
| 288 | 117.6 | 5.1 | 2450 | 3 | BC011409 | BC011409 | Homo sapi |
| 289 | 117.4 | 5.1 | 768 | 5 | BX876854 | BX876854 | BX876854 |
| c 290 | 117.2 | 5.1 | 1067 | 9 | CNS05HQH | AL337922 | Tetraodon |
| 291 | 116.6 | 5.0 | 738 | 6 | CB418995 | CB418995 | 591831 MA |
| 292 | 115.4 | 5.0 | 619 | 9 | FR0007657 | Z91467 | F.rubripes |
| 293 | 115.4 | 5.0 | 962 | 4 | BG969620 | BG969620 | 602836951 |

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|-------|-------|-----|------|---|----------|----------|-----------|
| 294 | 115 | 5.0 | 615 | 1 | AL803499 | AL803499 | AL803499 |
| 295 | 115 | 5.0 | 1030 | 5 | BQ714919 | BQ714919 | AGENCOURT |
| 296 | 114.4 | 4.9 | 704 | 6 | CB518006 | CB518006 | ssalrgb53 |
| 297 | 114 | 4.9 | 2079 | 6 | CD013998 | CD013998 | 90117389 |
| 298 | 113.8 | 4.9 | 634 | 6 | CB955397 | CB955397 | AGENCOURT |
| 299 | 113.8 | 4.9 | 1005 | 4 | BG167171 | BG167171 | 602344696 |
| 300 | 113.4 | 4.9 | 618 | 1 | AL787677 | AL787677 | AL787677 |
| 301 | 113.4 | 4.9 | 633 | 1 | AL789572 | AL789572 | AL789572 |
| 302 | 113.4 | 4.9 | 759 | 4 | BJ730921 | BJ730921 | BJ730921 |
| 303 | 113 | 4.9 | 677 | 7 | CK981590 | CK981590 | 4114067 B |
| 304 | 113 | 4.9 | 1570 | 3 | CR646752 | CR646752 | Tetraodon |
| 305 | 112.8 | 4.9 | 685 | 4 | BJ495916 | BJ495916 | BJ495916 |
| 306 | 112.4 | 4.8 | 774 | 7 | CO423341 | CO423341 | GGEZHT100 |
| 307 | 111.6 | 4.8 | 513 | 2 | BF105272 | BF105272 | 601822259 |
| 308 | 111.4 | 4.8 | 606 | 6 | CB581397 | CB581397 | AMGNNUC:C |
| 309 | 111.4 | 4.8 | 2394 | 3 | BC043491 | BC043491 | Homo sapi |
| c 310 | 111 | 4.8 | 1126 | 7 | CO645680 | CO645680 | ILLUMIGEN |
| 311 | 110.8 | 4.8 | 605 | 6 | CB581581 | CB581581 | AMGNNUC:N |
| 312 | 110.6 | 4.8 | 977 | 4 | BI331895 | BI331895 | 602982580 |
| 313 | 110.4 | 4.8 | 691 | 8 | AZ614547 | AZ614547 | 1M0443J19 |
| 314 | 110.4 | 4.8 | 1770 | 3 | CR644097 | CR644097 | Tetraodon |
| 315 | 109.4 | 4.7 | 510 | 6 | CB286305 | CB286305 | CMD34_E11 |
| 316 | 109.2 | 4.7 | 410 | 2 | AW226896 | AW226896 | um63b09.y |
| 317 | 109.2 | 4.7 | 848 | 7 | CN986271 | CN986271 | 61879_125 |
| 318 | 108.4 | 4.7 | 867 | 7 | CN172607 | CN172607 | AGENCOURT |
| 319 | 107.8 | 4.6 | 514 | 6 | CB286306 | CB286306 | CMD34_E12 |
| 320 | 107.4 | 4.6 | 673 | 6 | CA042007 | CA042007 | ssalplnb5 |
| 321 | 107.2 | 4.6 | 685 | 5 | BU136075 | BU136075 | 603124201 |
| 322 | 107.2 | 4.6 | 839 | 7 | CF249906 | CF249906 | esa006_a0 |
| c 323 | 107.2 | 4.6 | 861 | 7 | CN159685 | CN159685 | 948778_MA |
| 324 | 107.2 | 4.6 | 970 | 5 | BU122351 | BU122351 | 603146762 |
| 325 | 107.2 | 4.6 | 988 | 5 | BU122681 | BU122681 | 603149059 |
| c 326 | 106.8 | 4.6 | 584 | 1 | AL793872 | AL793872 | AL793872 |
| c 327 | 106.2 | 4.6 | 840 | 4 | BJ746350 | BJ746350 | BJ746350 |
| 328 | 106.2 | 4.6 | 888 | 9 | AY418357 | AY418357 | Pan trogl |
| 329 | 106 | 4.6 | 674 | 7 | CK948396 | CK948396 | 4073279 B |
| c 330 | 105.8 | 4.6 | 580 | 8 | AQ059652 | AQ059652 | CIT-HSP-2 |
| 331 | 105.4 | 4.5 | 751 | 5 | BP452350 | BP452350 | BP452350 |
| 332 | 104.8 | 4.5 | 700 | 6 | CB497940 | CB497940 | omykrbhb0 |
| 333 | 104.6 | 4.5 | 383 | 2 | AW107617 | AW107617 | ul93c02.y |
| 334 | 104.6 | 4.5 | 653 | 6 | CD309485 | CD309485 | StrPu691. |
| 335 | 104.4 | 4.5 | 677 | 7 | CK956169 | CK956169 | 4096235 B |
| 336 | 103.8 | 4.5 | 835 | 4 | BI757311 | BI757311 | 603029525 |
| 337 | 103.6 | 4.5 | 613 | 1 | AL679732 | AL679732 | AL679732 |
| 338 | 103.4 | 4.5 | 652 | 6 | CA343408 | CA343408 | 673504 NC |
| c 339 | 102.8 | 4.4 | 1188 | 6 | CD505366 | CD505366 | CDA73-C09 |
| 340 | 102.6 | 4.4 | 651 | 4 | BJ094864 | BJ094864 | BJ094864 |
| c 341 | 102 | 4.4 | 673 | 4 | BJ640772 | BJ640772 | BJ640772 |
| c 342 | 101.8 | 4.4 | 310 | 5 | BX636608 | BX636608 | BX636608 |
| 343 | 101.8 | 4.4 | 701 | 1 | AL133897 | AL133897 | DKFZp761K |
| 344 | 101.6 | 4.4 | 492 | 4 | BG970195 | BG970195 | 602839368 |
| 345 | 101.6 | 4.4 | 2202 | 3 | AK002629 | AK002629 | Mus muscu |
| 346 | 101.4 | 4.4 | 781 | 1 | AI529761 | AI529761 | ui82b06.y |
| 347 | 101 | 4.4 | 652 | 4 | BJ624350 | BJ624350 | BJ624350 |
| 348 | 101 | 4.4 | 879 | 7 | CO774398 | CO774398 | ILLUMIGEN |
| 349 | 101 | 4.4 | 1101 | 9 | CNS059KU | AL327351 | Tetraodon |
| 350 | 100.8 | 4.3 | 315 | 1 | AA104237 | AA104237 | mp01b01.r |

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|-------|-------|-----|------|---|----------|----------|-----------|
| 351 | 100.8 | 4.3 | 588 | 5 | BP448488 | BP448488 | BP448488 |
| 352 | 100.8 | 4.3 | 615 | 5 | BP449052 | BP449052 | BP449052 |
| 353 | 100.8 | 4.3 | 794 | 4 | BG575052 | BG575052 | 602598159 |
| 354 | 100.8 | 4.3 | 913 | 7 | CO579137 | CO579137 | ILLUMIGEN |
| 355 | 100 | 4.3 | 974 | 7 | CO579983 | CO579983 | ILLUMIGEN |
| 356 | 100 | 4.3 | 996 | 5 | BQ714776 | BQ714776 | AGENCOURT |
| 357 | 99 | 4.3 | 617 | 4 | BJ615347 | BJ615347 | BJ615347 |
| 358 | 98.6 | 4.2 | 708 | 4 | BJ731220 | BJ731220 | BJ731220 |
| 359 | 98.6 | 4.2 | 708 | 7 | CV527312 | CV527312 | CS_GIL_14 |
| 360 | 98.6 | 4.2 | 750 | 5 | BP448650 | BP448650 | BP448650 |
| 361 | 98.6 | 4.2 | 1022 | 5 | BM925650 | BM925650 | AGENCOURT |
| 362 | 98.4 | 4.2 | 564 | 6 | CA347839 | CA347839 | 679020 NC |
| 363 | 98.4 | 4.2 | 2306 | 3 | BC012716 | BC012716 | Mus muscu |
| 364 | 98.2 | 4.2 | 759 | 4 | BI330877 | BI330877 | 602981265 |
| 365 | 98.2 | 4.2 | 790 | 7 | CO555662 | CO555662 | AGENCOURT |
| c 366 | 98.2 | 4.2 | 808 | 4 | BJ716530 | BJ716530 | BJ716530 |
| c 367 | 98 | 4.2 | 834 | 4 | BJ746664 | BJ746664 | BJ746664 |
| 368 | 97.8 | 4.2 | 710 | 2 | BB667498 | BB667498 | BB667498 |
| c 369 | 97.6 | 4.2 | 761 | 1 | AI118428 | AI118428 | ue40e09.x |
| 370 | 97.4 | 4.2 | 656 | 5 | BQ388290 | BQ388290 | NISC_mn28 |
| 371 | 97.4 | 4.2 | 728 | 6 | CD493117 | CD493117 | CDA03-C12 |
| 372 | 97.4 | 4.2 | 807 | 5 | BU901536 | BU901536 | AGENCOURT |
| 373 | 97.4 | 4.2 | 921 | 7 | CN065626 | CN065626 | D15_Ag2_p |
| 374 | 97.2 | 4.2 | 697 | 2 | BB667336 | BB667336 | BB667336 |
| 375 | 97.2 | 4.2 | 697 | 4 | BG747143 | BG747143 | 602704364 |
| 376 | 97 | 4.2 | 874 | 7 | CN985398 | CN985398 | 58371_126 |
| 377 | 96.6 | 4.2 | 581 | 1 | AL791968 | AL791968 | AL791968 |
| c 378 | 96.6 | 4.2 | 639 | 2 | BF322562 | BF322562 | maa28e12. |
| 379 | 96.4 | 4.2 | 654 | 4 | BJ060547 | BJ060547 | BJ060547 |
| c 380 | 96.4 | 4.2 | 861 | 7 | CK974452 | CK974452 | 4105352 B |
| 381 | 96.4 | 4.2 | 871 | 5 | BQ900474 | BQ900474 | AGENCOURT |
| 382 | 96.4 | 4.2 | 913 | 5 | BQ714368 | BQ714368 | AGENCOURT |
| 383 | 96.4 | 4.2 | 938 | 5 | BQ942682 | BQ942682 | AGENCOURT |
| 384 | 96 | 4.1 | 643 | 7 | CV222277 | CV222277 | Le_mx0_58 |
| c 385 | 96 | 4.1 | 896 | 7 | CN159120 | CN159120 | 948155 MA |
| 386 | 95.6 | 4.1 | 603 | 6 | CB163625 | CB163625 | K-EST0224 |
| 387 | 95.6 | 4.1 | 662 | 1 | AL792519 | AL792519 | AL792519 |
| 388 | 95.6 | 4.1 | 665 | 1 | AL638480 | AL638480 | AL638480 |
| 389 | 95.4 | 4.1 | 573 | 1 | AL789331 | AL789331 | AL789331 |
| 390 | 95.4 | 4.1 | 1131 | 2 | BF687385 | BF687385 | 602102551 |
| 391 | 95.2 | 4.1 | 611 | 7 | CF250034 | CF250034 | esa007_f0 |
| 392 | 95.2 | 4.1 | 1005 | 2 | BE870911 | BE870911 | 601448862 |
| 393 | 95 | 4.1 | 430 | 2 | BB847324 | BB847324 | BB847324 |
| c 394 | 95 | 4.1 | 739 | 7 | CO387359 | CO387359 | AGENCOURT |
| 395 | 94.8 | 4.1 | 557 | 2 | AW318536 | AW318536 | um98f10.y |
| 396 | 94.6 | 4.1 | 573 | 7 | CO298247 | CO298247 | EK172617. |
| c 397 | 94.6 | 4.1 | 598 | 1 | AI303476 | AI303476 | ui71e01.x |
| c 398 | 94.4 | 4.1 | 555 | 1 | AI265736 | AI265736 | uj05f12.x |
| 399 | 94.4 | 4.1 | 934 | 2 | BF786200 | BF786200 | 602110490 |
| 400 | 94.2 | 4.1 | 415 | 1 | AI959352 | AI959352 | fd08e07.y |
| 401 | 94.2 | 4.1 | 561 | 7 | CN227962 | CN227962 | RJB035D05 |
| 402 | 94.2 | 4.1 | 582 | 6 | CA386855 | CA386855 | 668573 NC |
| 403 | 94.2 | 4.1 | 650 | 7 | CV041502 | CV041502 | 4139371 B |
| 404 | 94.2 | 4.1 | 666 | 6 | CA348546 | CA348546 | 679900 NC |
| 405 | 94.2 | 4.1 | 668 | 6 | CA349227 | CA349227 | 619554 NC |
| 406 | 93.8 | 4.0 | 415 | 5 | BY006441 | BY006441 | BY006441 |
| 407 | 93.8 | 4.0 | 424 | 2 | BB844926 | BB844926 | BB844926 |

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|-------|------|-----|------|---|-----------|----------|-------------|----|
| 408 | 93.8 | 4.0 | 554 | 2 | BE013295 | BE013295 | 123199 | MA |
| 409 | 93.8 | 4.0 | 1192 | 2 | BF789664 | BF789664 | 602105279 | |
| 410 | 93.6 | 4.0 | 718 | 5 | BX876842 | BX876842 | BX876842 | |
| 411 | 93.6 | 4.0 | 724 | 5 | BX875102 | BX875102 | BX875102 | |
| 412 | 93.6 | 4.0 | 755 | 5 | BX889578 | BX889578 | BX889578 | |
| 413 | 93.6 | 4.0 | 759 | 5 | BX885634 | BX885634 | BX885634 | |
| 414 | 93 | 4.0 | 690 | 8 | AZ614319 | AZ614319 | 1M0443N05 | |
| c 415 | 93 | 4.0 | 728 | 7 | CN585956 | CN585956 | USDA-FP_1 | |
| 416 | 93 | 4.0 | 746 | 2 | BF688309 | BF688309 | 602185172 | |
| c 417 | 93 | 4.0 | 822 | 7 | CN761092 | CN761092 | ID0AAA2BE | |
| 418 | 92.8 | 4.0 | 581 | 5 | BP275541 | BP275541 | BP275541 | |
| 419 | 92.8 | 4.0 | 753 | 7 | CK029964 | CK029964 | AGENCOURT | |
| 420 | 92.8 | 4.0 | 777 | 7 | CO573842 | CO573842 | AGENCOURT | |
| 421 | 92.6 | 4.0 | 547 | 7 | CR751755 | CR751755 | DKFZp469C | |
| c 422 | 92.6 | 4.0 | 774 | 7 | CF343072 | CF343072 | AGENCOURT | |
| 423 | 92.4 | 4.0 | 616 | 6 | CB163341 | CB163341 | K-EST0224 | |
| 424 | 91.6 | 3.9 | 356 | 5 | BY005600 | BY005600 | BY005600 | |
| 425 | 91.6 | 3.9 | 776 | 4 | BI103442 | BI103442 | 602888971 | |
| 426 | 91.2 | 3.9 | 572 | 2 | AW917402 | AW917402 | EST348706 | |
| 427 | 91.2 | 3.9 | 722 | 6 | CB951410 | CB951410 | AGENCOURT | |
| 428 | 91 | 3.9 | 535 | 1 | AL911920 | AL911920 | AL911920 | |
| c 429 | 91 | 3.9 | 551 | 4 | BJ021349 | BJ021349 | BJ021349 | |
| 430 | 91 | 3.9 | 606 | 4 | BJ009417 | BJ009417 | BJ009417 | |
| c 431 | 91 | 3.9 | 674 | 4 | BJ020682 | BJ020682 | BJ020682 | |
| c 432 | 91 | 3.9 | 687 | 4 | BJ019313 | BJ019313 | BJ019313 | |
| c 433 | 91 | 3.9 | 733 | 4 | BJ516248 | BJ516248 | BJ516248 | |
| c 434 | 91 | 3.9 | 753 | 4 | BJ518554 | BJ518554 | BJ518554 | |
| c 435 | 91 | 3.9 | 756 | 4 | BJ533312 | BJ533312 | BJ533312 | |
| 436 | 90.8 | 3.9 | 667 | 7 | CK947903 | CK947903 | 4072727 B | |
| 437 | 90.8 | 3.9 | 670 | 7 | CN793669 | CN793669 | 4128731 B | |
| 438 | 90.8 | 3.9 | 732 | 7 | CK967438 | CK967438 | 4082607 B | |
| 439 | 90.6 | 3.9 | 599 | 4 | BJ493042 | BJ493042 | BJ493042 | |
| 440 | 90.6 | 3.9 | 616 | 4 | BJ501742 | BJ501742 | BJ501742 | |
| 441 | 90.6 | 3.9 | 910 | 7 | CN992653 | CN992653 | 70709_125 | |
| c 442 | 90.4 | 3.9 | 732 | 3 | CNS08LE2 | BX017142 | Single re | |
| c 443 | 90.2 | 3.9 | 811 | 6 | CD632277 | CD632277 | 56066634J | |
| c 444 | 90 | 3.9 | 643 | 1 | AI785430 | AI785430 | uj42b06.x | |
| c 445 | 90 | 3.9 | 725 | 4 | BJ518275 | BJ518275 | BJ518275 | |
| 446 | 89.8 | 3.9 | 958 | 4 | BG167110 | BG167110 | 602344612 | |
| c 447 | 89.8 | 3.9 | 1125 | 9 | CNS03SJZ | AL258632 | Tetraodon | |
| 448 | 89.6 | 3.9 | 969 | 4 | BG291839 | BG291839 | 602386068 | |
| 449 | 89.4 | 3.9 | 904 | 5 | BU121683 | BU121683 | 603145755 | |
| 450 | 89.4 | 3.9 | 905 | 7 | CN173591 | CN173591 | AGENCOURT | |
| c 451 | 89.2 | 3.8 | 674 | 7 | CO704930 | CO704930 | DG32-292d | |
| c 452 | 89 | 3.8 | 127 | 2 | BF514925 | BF514925 | UI-H-BW1- | |
| 453 | 88.8 | 3.8 | 624 | 7 | CN275923 | CN275923 | ..170004245 | |
| 454 | 88.8 | 3.8 | 975 | 2 | BF533975 | BF533975 | 602075137 | |
| c 455 | 88.4 | 3.8 | 602 | 3 | CNS08M60 | BX018148 | Single re | |
| 456 | 88.2 | 3.8 | 398 | 5 | BY006400 | BY006400 | BY006400 | |
| c 457 | 88.2 | 3.8 | 823 | 2 | BF689099 | BF689099 | 602185172 | |
| 458 | 88.2 | 3.8 | 831 | 6 | CD105882 | CD105882 | AGENCOURT | |
| 459 | 88 | 3.8 | 812 | 4 | BI221130 | BI221130 | 602939634 | |
| 460 | 87.8 | 3.8 | 618 | 9 | FR0007653 | Z91463 | F.rubripes | |
| 461 | 87.8 | 3.8 | 891 | 4 | BG189133 | BG189133 | RST8173 A | |
| 462 | 87.4 | 3.8 | 510 | 5 | BX483530 | BX483530 | DKFZp686C | |
| 463 | 87.4 | 3.8 | 1201 | 9 | CNS015XW | AL106046 | Drosophil | |
| 464 | 87.2 | 3.8 | 579 | 5 | BP277054 | BP277054 | BP277054 | |

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|-------|------|-----|------|---|-----------|----------|-----------|
| 465 | 87 | 3.8 | 812 | 5 | BU364284 | BU364284 | 603584620 |
| 466 | 86.8 | 3.7 | 447 | 5 | BX618498 | BX618498 | BX618498 |
| c 467 | 86.8 | 3.7 | 615 | 7 | CK133545 | CK133545 | RE29447.3 |
| 468 | 86.4 | 3.7 | 830 | 4 | BG195984 | BG195984 | RST15067 |
| 469 | 86.2 | 3.7 | 550 | 1 | AI097692 | AI097692 | ue35b11.y |
| c 470 | 86.2 | 3.7 | 658 | 6 | CB503528 | CB503528 | ssalmge50 |
| 471 | 86 | 3.7 | 794 | 4 | BI328333 | BI328333 | 602985653 |
| c 472 | 85.6 | 3.7 | 548 | 7 | CO698361 | CO698361 | DG32-135b |
| c 473 | 85.4 | 3.7 | 618 | 9 | FR0049525 | AL605334 | Fugu rubr |
| 474 | 85.2 | 3.7 | 529 | 6 | CB224174 | CB224174 | 1JEJ32C4 |
| 475 | 85 | 3.7 | 1044 | 9 | CNS044X4 | AL274657 | Tetraodon |
| c 476 | 84.8 | 3.7 | 659 | 7 | CK132607 | CK132607 | RE03265.3 |
| 477 | 84.6 | 3.6 | 688 | 7 | CK977467 | CK977467 | 4108686 B |
| 478 | 84.4 | 3.6 | 416 | 7 | CF919654 | CF919654 | Bflor531. |
| 479 | 84.4 | 3.6 | 455 | 4 | BI387360 | BI387360 | BFL26_002 |
| 480 | 84.4 | 3.6 | 551 | 4 | BI442788 | BI442788 | dai90a05. |
| 481 | 84.4 | 3.6 | 702 | 5 | BU038648 | BU038648 | DH02E04 H |
| 482 | 84.2 | 3.6 | 581 | 5 | BP360001 | BP360001 | BP360001 |
| 483 | 84.2 | 3.6 | 788 | 5 | BX624452 | BX624452 | BX624452 |
| 484 | 84 | 3.6 | 303 | 7 | CR738701 | CR738701 | CR738701 |
| c 485 | 84 | 3.6 | 607 | 7 | CK132585 | CK132585 | RE02574.3 |
| 486 | 83.8 | 3.6 | 428 | 5 | BY006488 | BY006488 | BY006488 |
| 487 | 83.6 | 3.6 | 840 | 5 | BX624575 | BX624575 | BX624575 |
| c 488 | 83.2 | 3.6 | 708 | 5 | BQ202033 | BQ202033 | UI-R-EB1- |
| 489 | 83 | 3.6 | 660 | 6 | CD703965 | CD703965 | EST20492 |
| 490 | 83 | 3.6 | 1068 | 5 | BU145928 | BU145928 | AGENCOURT |
| 491 | 82.6 | 3.6 | 728 | 4 | BG569536 | BG569536 | 602588811 |
| 492 | 82.4 | 3.6 | 736 | 7 | CK950173 | CK950173 | 4075687 B |
| 493 | 82.2 | 3.5 | 625 | 7 | CK951591 | CK951591 | 4090903 B |
| 494 | 82.2 | 3.5 | 1016 | 9 | CNS03VYT | AL263054 | Tetraodon |
| 495 | 81.6 | 3.5 | 666 | 4 | BG971005 | BG971005 | 602840033 |
| 496 | 81.4 | 3.5 | 557 | 2 | BF080461 | BF080461 | 231360 MA |
| c 497 | 81.2 | 3.5 | 656 | 2 | AW338024 | AW338024 | xw65c05.x |
| c 498 | 81.2 | 3.5 | 1080 | 9 | CNS03FCV | AL241528 | Tetraodon |
| 499 | 81 | 3.5 | 551 | 6 | CD331938 | CD331938 | StrPu537. |
| c 500 | 81 | 3.5 | 638 | 7 | CK950104 | CK950104 | 4075303 B |
| 501 | 80.8 | 3.5 | 789 | 7 | CO808016 | CO808016 | AGENCOURT |
| 502 | 80.4 | 3.5 | 863 | 7 | CK974673 | CK974673 | 4105736 B |
| 503 | 80.2 | 3.5 | 1100 | 5 | BQ278891 | BQ278891 | AGENCOURT |
| 504 | 79.6 | 3.4 | 578 | 7 | CK888307 | CK888307 | SGP149514 |
| 505 | 79.4 | 3.4 | 696 | 4 | BG971909 | BG971909 | 602841666 |
| 506 | 79.4 | 3.4 | 886 | 4 | BG402016 | BG402016 | 602466734 |
| 507 | 79.2 | 3.4 | 651 | 7 | CO259652 | CO259652 | 4131159 B |
| 508 | 79.2 | 3.4 | 842 | 7 | CO246322 | CO246322 | AGENCOURT |
| c 509 | 79 | 3.4 | 514 | 1 | AI132717 | AI132717 | ue33h09.x |
| 510 | 79 | 3.4 | 707 | 7 | CO641589 | CO641589 | USDA-FP_1 |
| 511 | 78.8 | 3.4 | 452 | 4 | BM090021 | BM090021 | 503910 MA |
| 512 | 78.8 | 3.4 | 642 | 6 | CB155303 | CB155303 | K-EST0213 |
| 513 | 78.8 | 3.4 | 759 | 7 | CN275924 | CN275924 | 170006008 |
| 514 | 78.6 | 3.4 | 328 | 5 | BY005676 | BY005676 | BY005676 |
| 515 | 78.6 | 3.4 | 823 | 4 | BG193837 | BG193837 | RST12973 |
| 516 | 78 | 3.4 | 801 | 4 | BG212458 | BG212458 | RST32045 |
| 517 | 77.8 | 3.4 | 449 | 2 | BF080415 | BF080415 | 231292 MA |
| c 518 | 77.8 | 3.4 | 614 | 6 | CB169862 | CB169862 | KSV603161 |
| 519 | 77.6 | 3.3 | 441 | 9 | CNS07H5L | AL610635 | Anopheles |
| c 520 | 77.6 | 3.3 | 589 | 1 | AI256545 | AI256545 | ui87g04.x |
| c 521 | 77.6 | 3.3 | 592 | 7 | CK131146 | CK131146 | GH06505.3 |

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| | 522 | 77.2 | 3.3 | 425 | 4 | BJ624661 | BJ624661 | BJ624661 |
| | 523 | 77 | 3.3 | 1297 | 3 | AK078371 | AK078371 | Mus muscu |
| c | 524 | 76.6 | 3.3 | 538 | 6 | CD336301 | CD336301 | StrPu537. |
| c | 525 | 76.6 | 3.3 | 616 | 4 | BJ507779 | BJ507779 | BJ507779 |
| | 526 | 76.6 | 3.3 | 1107 | 5 | BM924331 | BM924331 | AGENCOURT |
| | 527 | 75.8 | 3.3 | 1118 | 2 | BF582087 | BF582087 | 602099271 |
| | 528 | 75.6 | 3.3 | 414 | 7 | CO994585 | CO994585 | UMC-pd12 |
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| | 530 | 75.6 | 3.3 | 652 | 4 | BJ705583 | BJ705583 | BJ705583 |
| | 531 | 75.6 | 3.3 | 739 | 7 | CO047895 | CO047895 | Lr_AT1CF |
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| | 533 | 75.2 | 3.2 | 792 | 2 | BF786091 | BF786091 | 602110662 |
| | 534 | 75.2 | 3.2 | 1110 | 2 | BF533824 | BF533824 | 602075352 |
| | 535 | 75 | 3.2 | 568 | 1 | AA212451 | AA212451 | mw76g12.r |
| | 536 | 75 | 3.2 | 648 | 7 | CN983881 | CN983881 | 52591_126 |
| c | 537 | 75 | 3.2 | 732 | 4 | BJ743004 | BJ743004 | BJ743004 |
| | 538 | 74.8 | 3.2 | 616 | 1 | AA255225 | AA255225 | mz85d04.r |
| | 539 | 74.6 | 3.2 | 494 | 4 | BJ623942 | BJ623942 | BJ623942 |
| | 540 | 74.6 | 3.2 | 557 | 6 | CB157680 | CB157680 | K-EST0216 |
| | 541 | 74.6 | 3.2 | 770 | 4 | BG201991 | BG201991 | RST21337 |
| | 542 | 74.2 | 3.2 | 694 | 1 | AU129743 | AU129743 | AU129743 |
| | 543 | 74.2 | 3.2 | 782 | 4 | BG167429 | BG167429 | 602342703 |
| | 544 | 74.2 | 3.2 | 812 | 1 | AI663013 | AI663013 | uj69f10.y |
| c | 545 | 74.2 | 3.2 | 915 | 3 | CNS08R35 | BX024525 | Single re |
| | 546 | 74 | 3.2 | 582 | 1 | AA075453 | AA075453 | zm87e07.r |
| | 547 | 73.8 | 3.2 | 778 | 7 | CF250901 | CF250901 | esa018_e0 |
| | 548 | 73.6 | 3.2 | 136 | 1 | AA073542 | AA073542 | mm94b03.r |
| | 549 | 73.2 | 3.2 | 508 | 2 | BF383473 | BF383473 | 602045154 |
| | 550 | 73.2 | 3.2 | 599 | 4 | BJ488432 | BJ488432 | BJ488432 |
| | 551 | 73.2 | 3.2 | 751 | 7 | CR769273 | CR769273 | DKFZp469I |
| | 552 | 73 | 3.1 | 533 | 2 | BF131143 | BF131143 | 601819955 |
| | 553 | 73 | 3.1 | 573 | 6 | CB161428 | CB161428 | K-EST0221 |
| | 554 | 73 | 3.1 | 837 | 7 | CN763566 | CN763566 | ID0AAA7BG |
| c | 555 | 73 | 3.1 | 980 | 1 | AI256260 | AI256260 | ui96h12.x |
| c | 556 | 72.8 | 3.1 | 517 | 2 | AW604423 | AW604423 | RC3-CT025 |
| c | 557 | 72.8 | 3.1 | 662 | 7 | CK948186 | CK948186 | 4072991 B |
| | 558 | 72.8 | 3.1 | 723 | 4 | BG424452 | BG424452 | 602447772 |
| c | 559 | 72.6 | 3.1 | 565 | 7 | CO328600 | CO328600 | EK291003. |
| | 560 | 72.6 | 3.1 | 741 | 7 | CR559577 | CR559577 | DKFZp459B |
| | 561 | 72.4 | 3.1 | 584 | 6 | CB586065 | CB586065 | AMGNNUC:N |
| | 562 | 72.4 | 3.1 | 935 | 2 | BF234991 | BF234991 | 602027544 |
| | 563 | 72.2 | 3.1 | 765 | 7 | CK959288 | CK959288 | 4100123 B |
| c | 564 | 72.2 | 3.1 | 781 | 4 | BJ748442 | BJ748442 | BJ748442 |
| | 565 | 72 | 3.1 | 361 | 5 | BY082449 | BY082449 | BY082449 |
| | 566 | 72 | 3.1 | 554 | 5 | BP243787 | BP243787 | BP243787 |
| | 567 | 72 | 3.1 | 560 | 5 | BX485008 | BX485008 | DKFZp686G |
| | 568 | 72 | 3.1 | 670 | 7 | CO641121 | CO641121 | USDA-FP_1 |
| | 569 | 72 | 3.1 | 775 | 4 | BI144659 | BI144659 | 602909950 |
| | 570 | 71.8 | 3.1 | 935 | 2 | BF532873 | BF532873 | 602074982 |
| c | 571 | 71.8 | 3.1 | 1028 | 9 | CNS046W3 | AL277212 | Tetraodon |
| | 572 | 71.6 | 3.1 | 729 | 5 | BQ179273 | BQ179273 | UI-M-EW0- |
| | 573 | 71.6 | 3.1 | 793 | 7 | CF662633 | CF662633 | CcLL03a11 |
| | 574 | 71.4 | 3.1 | 690 | 6 | CB467191 | CB467191 | 732919 MA |
| c | 575 | 71 | 3.1 | 430 | 4 | BI451798 | BI451798 | TY14E03 h |
| | 576 | 71 | 3.1 | 725 | 7 | CK349802 | CK349802 | hggfha18B |
| | 577 | 70.8 | 3.1 | 629 | 4 | BM791817 | BM791817 | K-EST0071 |
| c | 578 | 70.6 | 3.0 | 512 | 1 | AI265232 | AI265232 | ui97d02.x |

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| 579 | 70.4 | 3.0 | 680 | 5 | BX889196 | BX889196 | BX889196 |
| 580 | 70.4 | 3.0 | 871 | 7 | CN972726 | CN972726 | 20223_124 |
| 581 | 70.4 | 3.0 | 944 | 9 | CG770584 | CG770584 | TcB41.1_E |
| 582 | 70 | 3.0 | 689 | 4 | BM642521 | BM642521 | 170006873 |
| 583 | 70 | 3.0 | 733 | 7 | CO561098 | CO561098 | AGENCOURT |
| 584 | 69.8 | 3.0 | 547 | 7 | CR763995 | CR763995 | DKFZp469L |
| 585 | 69.8 | 3.0 | 688 | 4 | BG286763 | BG286763 | 602382611 |
| 586 | 69.6 | 3.0 | 353 | 5 | BY005597 | BY005597 | BY005597 |
| c 587 | 69.6 | 3.0 | 484 | 1 | AI265260 | AI265260 | ui97f08.x |
| 588 | 69.6 | 3.0 | 698 | 7 | CK450042 | CK450042 | 893658 MA |
| 589 | 69.4 | 3.0 | 563 | 4 | BM624521 | BM624521 | 170006874 |
| 590 | 69.4 | 3.0 | 722 | 5 | BX879296 | BX879296 | BX879296 |
| c 591 | 69.4 | 3.0 | 1199 | 6 | CD503770 | CD503770 | CDA64-C01 |
| 592 | 69.2 | 3.0 | 789 | 7 | CO558955 | CO558955 | AGENCOURT |
| c 593 | 69 | 3.0 | 315 | 5 | BY356244 | BY356244 | BY356244 |
| c 594 | 69 | 3.0 | 517 | 1 | AI118387 | AI118387 | ue36a02.x |
| c 595 | 68.8 | 3.0 | 498 | 1 | AI118135 | AI118135 | ue34c01.x |
| 596 | 68.8 | 3.0 | 515 | 2 | BB283598 | BB283598 | BB283598 |
| c 597 | 68.8 | 3.0 | 669 | 4 | BG203058 | BG203058 | RST22427 |
| 598 | 68.6 | 3.0 | 441 | 4 | BG876589 | BG876589 | QV1-DT006 |
| 599 | 68.6 | 3.0 | 614 | 4 | BM607789 | BM607789 | 170006870 |
| 600 | 68.6 | 3.0 | 837 | 7 | CN976403 | CN976403 | 26464_125 |
| 601 | 68.6 | 3.0 | 847 | 4 | BG400151 | BG400151 | 602440934 |
| 602 | 68.6 | 3.0 | 855 | 7 | CN977220 | CN977220 | 27419_125 |
| 603 | 68.4 | 2.9 | 446 | 1 | AL694265 | AL694265 | AL694265 |
| 604 | 68.2 | 2.9 | 428 | 8 | AQ194654 | AQ194654 | RPCI11-48 |
| c 605 | 68.2 | 2.9 | 480 | 1 | AI787349 | AI787349 | uj66f05.x |
| c 606 | 68.2 | 2.9 | 666 | 7 | CK838901 | CK838901 | UI-R-AC0- |
| 607 | 68 | 2.9 | 445 | 7 | CN750793 | CN750793 | ApDT-XXVI |
| 608 | 68 | 2.9 | 510 | 1 | AI386060 | AI386060 | mm15f04.y |
| 609 | 67.8 | 2.9 | 512 | 6 | CA380373 | CA380373 | 659644 NC |
| 610 | 67.8 | 2.9 | 563 | 7 | CK349927 | CK349927 | hggfha20A |
| 611 | 67.6 | 2.9 | 470 | 2 | BB747310 | BB747310 | BB747310 |
| c 612 | 67.6 | 2.9 | 672 | 6 | CA331021 | CA331021 | hab31b10. |
| 613 | 67.6 | 2.9 | 792 | 7 | CO573111 | CO573111 | AGENCOURT |
| c 614 | 67.2 | 2.9 | 588 | 6 | CB505187 | CB505187 | ssalmge50 |
| 615 | 67 | 2.9 | 400 | 7 | CN976669 | CN976669 | 26779_125 |
| c 616 | 67 | 2.9 | 692 | 9 | AG078157 | AG078157 | Pan trogl |
| 617 | 67 | 2.9 | 738 | 7 | CK474315 | CK474315 | AGENCOURT |
| c 618 | 66.6 | 2.9 | 535 | 7 | CO284467 | CO284467 | EK166132. |
| 619 | 66.6 | 2.9 | 616 | 2 | AW701598 | AW701598 | uq88b10.y |
| 620 | 66.6 | 2.9 | 631 | 4 | BJ004103 | BJ004103 | BJ004103 |
| 621 | 66.6 | 2.9 | 742 | 6 | CB952913 | CB952913 | AGENCOURT |
| 622 | 66.6 | 2.9 | 821 | 6 | CB200045 | CB200045 | AGENCOURT |
| 623 | 66.4 | 2.9 | 571 | 1 | AU243299 | AU243299 | AU243299 |
| 624 | 66.2 | 2.9 | 400 | 7 | CO261693 | CO261693 | 4134046 B |
| 625 | 66 | 2.8 | 611 | 6 | CA968819 | CA968819 | CcLL03a08 |
| 626 | 66 | 2.8 | 1447 | 7 | CV200634 | CV200634 | km06e10.y |
| c 627 | 65.6 | 2.8 | 618 | 9 | FR0007644 | Z91454 | F.rubripes |
| 628 | 65.6 | 2.8 | 901 | 7 | CN501635 | CN501635 | AGENCOURT |
| c 629 | 65.4 | 2.8 | 344 | 1 | AJ283854 | AJ283854 | 4A3B-AAG- |
| c 630 | 65.4 | 2.8 | 697 | 2 | AW942728 | AW942728 | LD25345.3 |
| 631 | 65.4 | 2.8 | 805 | 5 | BU124084 | BU124084 | 603147892 |
| 632 | 65.4 | 2.8 | 829 | 2 | BF782818 | BF782818 | 602107680 |
| 633 | 65.2 | 2.8 | 632 | 4 | BJ528642 | BJ528642 | BJ528642 |
| 634 | 65.2 | 2.8 | 762 | 1 | AA717701 | AA717701 | vp94g02.r |
| 635 | 65.2 | 2.8 | 903 | 7 | CN157171 | CN157171 | 945851 MA |

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| c 636 | 65 | 2.8 | 572 | 7 | CK604711 | CK604711 | UT01394.3 |
| 637 | 65 | 2.8 | 939 | 5 | BQ922613 | BQ922613 | AGENCOURT |
| 638 | 65 | 2.8 | 1109 | 6 | CD505365 | CD505365 | CDA73-C09 |
| 639 | 64.8 | 2.8 | 196 | 1 | AI317676 | AI317676 | uj22c05.y |
| 640 | 64.8 | 2.8 | 458 | 7 | CO265158 | CO265158 | EK141664. |
| 641 | 64.8 | 2.8 | 650 | 6 | CD596098 | CD596098 | RK100A2F1 |
| 642 | 64.8 | 2.8 | 713 | 6 | CA347838 | CA347838 | 679019 NC |
| c 643 | 64.8 | 2.8 | 815 | 1 | AA986709 | AA986709 | uc80d04.x |
| 644 | 64.6 | 2.8 | 759 | 4 | BJ728374 | BJ728374 | BJ728374 |
| 645 | 64.4 | 2.8 | 492 | 1 | AA493091 | AA493091 | vi71h01.r |
| 646 | 64.4 | 2.8 | 647 | 1 | AA880242 | AA880242 | vv98g03.r |
| 647 | 64.2 | 2.8 | 854 | 4 | BI147191 | BI147191 | 602913291 |
| 648 | 64 | 2.8 | 463 | 1 | AA895843 | AA895843 | vy34h02.r |
| 649 | 64 | 2.8 | 469 | 6 | CB147253 | CB147253 | K-EST0203 |
| c 650 | 64 | 2.8 | 489 | 1 | AA985955 | AA985955 | uc72h01.x |
| 651 | 64 | 2.8 | 512 | 1 | AL785003 | AL785003 | AL785003 |
| c 652 | 64 | 2.8 | 547 | 7 | CO696892 | CO696892 | DG32-1041 |
| 653 | 63.8 | 2.8 | 721 | 7 | CK663177 | CK663177 | A296 Symb |
| 654 | 63.8 | 2.8 | 891 | 4 | BG426822 | BG426822 | 602493003 |
| 655 | 63.8 | 2.8 | 966 | 2 | BF027320 | BF027320 | 601671692 |
| c 656 | 63.6 | 2.7 | 705 | 6 | CB165252 | CB165252 | ZDW602600 |
| 657 | 63.6 | 2.7 | 789 | 7 | CN174688 | CN174688 | AGENCOURT |
| 658 | 63.4 | 2.7 | 1716 | 6 | CD013997 | CD013997 | 90117357 |
| 659 | 63.2 | 2.7 | 364 | 5 | BX872852 | BX872852 | BX872852 |
| 660 | 63.2 | 2.7 | 729 | 7 | CO570100 | CO570100 | AGENCOURT |
| 661 | 63.2 | 2.7 | 950 | 7 | CO582747 | CO582747 | ILLUMIGEN |
| 662 | 63 | 2.7 | 1267 | 4 | BG210359 | BG210359 | RST29896 |
| c 663 | 62.8 | 2.7 | 556 | 2 | BE026512 | BE026512 | db27e05.x |
| 664 | 62.8 | 2.7 | 731 | 7 | CV434524 | CV434524 | CS_hyp_35 |
| 665 | 62.6 | 2.7 | 346 | 4 | BM030341 | BM030341 | 488958 MA |
| 666 | 62.6 | 2.7 | 494 | 8 | AQ620313 | AQ620313 | HS_5180_B |
| c 667 | 62.6 | 2.7 | 569 | 6 | CA342060 | CA342060 | 671852 NC |
| 668 | 62.4 | 2.7 | 638 | 4 | BM649075 | BM649075 | 170006873 |
| 669 | 62.4 | 2.7 | 807 | 7 | CK030429 | CK030429 | AGENCOURT |
| 670 | 62.4 | 2.7 | 886 | 2 | BF788242 | BF788242 | 602113469 |
| 671 | 62.4 | 2.7 | 980 | 4 | BG179775 | BG179775 | 602328862 |
| 672 | 62 | 2.7 | 352 | 9 | FR0049577 | AL605386 | Fugu rubr |
| 673 | 62 | 2.7 | 605 | 9 | FR0007158 | Z90968 | F.rubripes |
| c 674 | 62 | 2.7 | 624 | 4 | BG302826 | BG302826 | fl39e03.x |
| 675 | 62 | 2.7 | 952 | 5 | BU122907 | BU122907 | 603147125 |
| 676 | 61.8 | 2.7 | 630 | 6 | CB577476 | CB577476 | AMGNNUC:U |
| c 677 | 61.8 | 2.7 | 631 | 7 | CK132736 | CK132736 | RE07815.3 |
| 678 | 61.8 | 2.7 | 888 | 6 | CD759765 | CD759765 | AGENCOURT |
| c 679 | 61.6 | 2.7 | 504 | 7 | CO262072 | CO262072 | EK084327. |
| 680 | 61.6 | 2.7 | 613 | 1 | AA647358 | AA647358 | vp88c04.r |
| c 681 | 61.6 | 2.7 | 619 | 9 | FR0007662 | Z91472 | F.rubripes |
| c 682 | 61.4 | 2.6 | 483 | 9 | CL583901 | CL583901 | OB_Ba007 |
| 683 | 61.4 | 2.6 | 684 | 6 | CD341703 | CD341703 | StrPu536. |
| 684 | 61.4 | 2.6 | 852 | 6 | CA976637 | CA976637 | AGENCOURT |
| 685 | 61.2 | 2.6 | 368 | 5 | BU473251 | BU473251 | 603760179 |
| c 686 | 61.2 | 2.6 | 596 | 9 | FR0049628 | AL605437 | Fugu rubr |
| 687 | 61.2 | 2.6 | 623 | 7 | CK517693 | CK517693 | rswjb0_00 |
| 688 | 61 | 2.6 | 415 | 9 | FR0014950 | AL006159 | F.rubripe |
| 689 | 61 | 2.6 | 739 | 4 | BG195983 | BG195983 | RST15066 |
| 690 | 61 | 2.6 | 1071 | 5 | BU525573 | BU525573 | AGENCOURT |
| 691 | 60.8 | 2.6 | 638 | 4 | BI103514 | BI103514 | 602889055 |
| c 692 | 60.8 | 2.6 | 675 | 4 | BJ136139 | BJ136139 | BJ136139 |

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|-------|------|-----|-----|---|-----------|----------|------------|
| c 693 | 60.8 | 2.6 | 738 | 6 | CB659466 | CB659466 | OSJNEc16H |
| 694 | 60.8 | 2.6 | 806 | 1 | AI048638 | AI048638 | ud64c07.y |
| c 695 | 60.8 | 2.6 | 829 | 6 | CB666604 | CB666604 | OSJNEd13J |
| 696 | 60.6 | 2.6 | 491 | 4 | BG427032 | BG427032 | 602493934 |
| c 697 | 60.6 | 2.6 | 590 | 4 | BJ142883 | BJ142883 | BJ142883 |
| 698 | 60.6 | 2.6 | 641 | 7 | CF254125 | CF254125 | mdvn112_a |
| c 699 | 60.6 | 2.6 | 714 | 9 | AG578491 | AG578491 | Mus muscu |
| c 700 | 60.6 | 2.6 | 728 | 4 | BJ139199 | BJ139199 | BJ139199 |
| c 701 | 60.6 | 2.6 | 732 | 7 | CV516957 | CV516957 | 0048P0018 |
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| 703 | 60.4 | 2.6 | 581 | 1 | AA473690 | AA473690 | vg89c08.r |
| c 704 | 60.4 | 2.6 | 638 | 7 | CK940315 | CK940315 | 4113683 B |
| c 705 | 60.4 | 2.6 | 638 | 7 | CK955845 | CK955845 | 4095851 B |
| c 706 | 60.2 | 2.6 | 811 | 8 | BZ267251 | BZ267251 | CH230-262 |
| 707 | 60 | 2.6 | 495 | 1 | AA674349 | AA674349 | vp98h05.r |
| 708 | 60 | 2.6 | 784 | 9 | CL311817 | CL311817 | 286867_LB |
| 709 | 59.8 | 2.6 | 497 | 1 | AJ683303 | AJ683303 | AJ683303 |
| 710 | 59.8 | 2.6 | 546 | 1 | AA575452 | AA575452 | vl90b05.r |
| 711 | 59.8 | 2.6 | 552 | 1 | AI286386 | AI286386 | ui75g08.y |
| 712 | 59.8 | 2.6 | 728 | 7 | CO641072 | CO641072 | USDA-FP_1 |
| 713 | 59.6 | 2.6 | 379 | 1 | AV683166 | AV683166 | AV683166 |
| 714 | 59.6 | 2.6 | 399 | 7 | T62130 | T62130 | yc66ell.r1 |
| 715 | 59.6 | 2.6 | 997 | 9 | CNS005TE | AL060767 | Drosophil |
| c 716 | 59.4 | 2.6 | 605 | 7 | CK604610 | CK604610 | UT01321.3 |
| c 717 | 59.4 | 2.6 | 650 | 9 | CL196913 | CL196913 | 104_423_1 |
| 718 | 59.4 | 2.6 | 681 | 7 | CN790431 | CN790431 | 4125029_B |
| c 719 | 59.4 | 2.6 | 815 | 9 | CG231386 | CG231386 | OGWGN83TH |
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| c 730 | 58.6 | 2.5 | 481 | 1 | AI668249 | AI668249 | 605018G07 |
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| c 732 | 58.6 | 2.5 | 493 | 1 | AI664846 | AI664846 | 605002D07 |
| c 733 | 58.6 | 2.5 | 522 | 1 | AI759125 | AI759125 | 605085D09 |
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| c 735 | 58.6 | 2.5 | 569 | 6 | CA399837 | CA399837 | EL01N0326 |
| c 736 | 58.6 | 2.5 | 572 | 6 | CA404541 | CA404541 | EL01N0519 |
| 737 | 58.6 | 2.5 | 618 | 2 | AW065890 | AW065890 | 687002E04 |
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| c 740 | 58.6 | 2.5 | 656 | 6 | CD446879 | CD446879 | EL01T0208 |
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| c 742 | 58.6 | 2.5 | 683 | 4 | BJ816482 | BJ816482 | BJ816482 |
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| c 744 | 58.6 | 2.5 | 720 | 6 | CA399209 | CA399209 | EL01N0315 |
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| c 750 | 58.6 | 2.5 | 785 | 6 | CD446551 | CD446551 | EL01T0203 |
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| 778 | 57 | 2.5 | 1101 | 9 | CNS00KFD | AL077908 | Drosophil |
| 779 | 56.8 | 2.4 | 440 | 2 | BB745467 | BB745467 | BB745467 |
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| c 789 | 56.6 | 2.4 | 628 | 8 | CC386449 | CC386449 | PUHPE49TB |
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| c 799 | 56.2 | 2.4 | 426 | 7 | CO308066 | CO308066 | EK256548. |
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| c 801 | 56.2 | 2.4 | 793 | 4 | BJ149397 | BJ149397 | BJ149397 |
| 802 | 56.2 | 2.4 | 809 | 4 | BG971667 | BG971667 | 602840766 |
| 803 | 56.2 | 2.4 | 1101 | 9 | CNS000WU | AL053681 | Drosophil |
| 804 | 56 | 2.4 | 436 | 7 | CO316063 | CO316063 | EK263564. |
| 805 | 56 | 2.4 | 488 | 3 | AY432118 | AY432118 | Aedes aeg |
| c 806 | 56 | 2.4 | 504 | 9 | CG801172 | CG801172 | 1118018D0 |

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| 807 | 56 | 2.4 | 568 | 5 | BP213630 | BP213630 | BP213630 |
| c 808 | 56 | 2.4 | 695 | 4 | BJ776790 | BJ776790 | BJ776790 |
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| 811 | 55.8 | 2.4 | 221 | 2 | BB561857 | BB561857 | BB561857 |
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| c 818 | 55.6 | 2.4 | 454 | 4 | BJ817721 | BJ817721 | BJ817721 |
| 819 | 55.6 | 2.4 | 521 | 4 | BM130311 | BM130311 | pb29d12.y |
| 820 | 55.6 | 2.4 | 525 | 2 | BE138067 | BE138067 | ug48a07.y |
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| 825 | 55.6 | 2.4 | 813 | 6 | CA480775 | CA480775 | AGENCOURT |
| 826 | 55.6 | 2.4 | 984 | 9 | CNS006LF | AL065715 | Drosophil |
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| c 828 | 55.4 | 2.4 | 309 | 9 | CL583240 | CL583240 | OB_Ba004 |
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| 835 | 54.8 | 2.4 | 570 | 5 | BP257713 | BP257713 | BP257713 |
| c 836 | 54.8 | 2.4 | 573 | 9 | FR0049536 | AL605345 | Fugu rubr |
| c 837 | 54.8 | 2.4 | 619 | 9 | FR0015778 | AL006985 | F.rubripe |
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| 840 | 54.6 | 2.4 | 603 | 5 | BX499005 | BX499005 | DKFZp779A |
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| 852 | 54.2 | 2.3 | 576 | 4 | BJ525957 | BJ525957 | BJ525957 |
| 853 | 54.2 | 2.3 | 628 | 2 | BF787599 | BF787599 | 602114528 |
| 854 | 54.2 | 2.3 | 1194 | 7 | CV186196 | CV186196 | A-013 D. |
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| 857 | 54 | 2.3 | 580 | 5 | BP215685 | BP215685 | BP215685 |
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| c 864 | 53.6 | 2.3 | 816 | 7 | CR530976 | CR530976 | CR530976 |
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| c 868 | 53.6 | 2.3 | 1014 | 9 | CNS05PJQ | AL348047 | Tetraodon |
| c 869 | 53.4 | 2.3 | 253 | 2 | AW531318 | AW531318 | UI-R-C4-a |
| c 870 | 53.4 | 2.3 | 360 | 9 | FR0015823 | AL007029 | F.rubripe |
| 871 | 53.4 | 2.3 | 574 | 7 | CN133765 | CN133765 | OX1_18_E0 |
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| 874 | 53.4 | 2.3 | 733 | 9 | CR501049 | CR501049 | Medicago |
| 875 | 53.4 | 2.3 | 736 | 9 | CR500903 | CR500903 | Medicago |
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| c 882 | 53.2 | 2.3 | 552 | 2 | AW351201 | AW351201 | GM210011A |
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| 889 | 53.2 | 2.3 | 873 | 7 | CN167653 | CN167653 | AGENCOURT |
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| 899 | 52.8 | 2.3 | 652 | 8 | AZ945505 | AZ945505 | 2M0206H23 |
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| c 901 | 52.8 | 2.3 | 755 | 4 | BJ809035 | BJ809035 | BJ809035 |
| c 902 | 52.6 | 2.3 | 573 | 8 | AZ831866 | AZ831866 | 2M0111C19 |
| 903 | 52.6 | 2.3 | 619 | 9 | FR0007177 | Z90987 | F.rubripes |
| 904 | 52.6 | 2.3 | 992 | 9 | CNS038FN | AL232556 | Tetraodon |
| c 905 | 52.4 | 2.3 | 464 | 9 | CC693642 | CC693642 | OGUGK52TH |
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| c 908 | 52.4 | 2.3 | 528 | 7 | CV051393 | CV051393 | EST 10848 |
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| 912 | 52.4 | 2.3 | 573 | 7 | CV053322 | CV053322 | EST 12770 |
| 913 | 52.4 | 2.3 | 593 | 7 | CV053078 | CV053078 | EST 12526 |
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| c 918 | 52.2 | 2.3 | 443 | 8 | CC029515 | CC029515 | 3591_1_11 |
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| 921 | 52 | 2.2 | 343 | 4 | BG182337 | BG182337 | RST1203_A |
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| 924 | 52 | 2.2 | 631 | 6 | CA111498 | CA111498 | SCAGLB107 |
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| 927 | 52 | 2.2 | 803 | 1 | AJ006537 | AJ006537 | AJ006537 |
| c 928 | 51.8 | 2.2 | 496 | 1 | AI855338 | AI855338 | 603014F06 |
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| 940 | 51.8 | 2.2 | 748 | 6 | CB954704 | CB954704 | AGENCOURT |
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| 950 | 51.8 | 2.2 | 1419 | 9 | CL965868 | CL965868 | OsIFCC012 |
| c 951 | 51.6 | 2.2 | 335 | 8 | CC040482 | CC040482 | 3591_1_13 |
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| c 963 | 51.6 | 2.2 | 777 | 9 | CG267261 | CG267261 | OGWHF51TH |
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| c 974 | 51.4 | 2.2 | 673 | 4 | BJ783526 | BJ783526 | BJ783526 |
| 975 | 51.4 | 2.2 | 673 | 9 | CL537275 | CL537275 | OB_Ba004 |
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| c 978 | 51.4 | 2.2 | 702 | 4 | BJ788990 | BJ788990 | BJ788990 |
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| c 981 | 51.4 | 2.2 | 709 | 4 | BJ818107 | BJ818107 | BJ818107 |
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| 985 | 51.4 | 2.2 | 1127 | 7 | CK028276 | CK028276 | AGENCOURT |
| 986 | 51.2 | 2.2 | 532 | 9 | CC733695 | CC733695 | OGUCO18TH |
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| c 988 | 51.2 | 2.2 | 562 | 9 | CC733706 | CC733706 | OGUCO18TV |
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| c1008 | 51 | 2.2 | 812 | 6 | CB671618 | CB671618 | OSJNEe05E |
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| 1011 | 50.8 | 2.2 | 265 | 7 | CV052826 | CV052826 | EST 12274 |
| c1012 | 50.8 | 2.2 | 494 | 7 | CV047765 | CV047765 | EST 13082 |
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| c1018 | 50.8 | 2.2 | 647 | 4 | BM269408 | BM269408 | MEST409-F |
| c1019 | 50.8 | 2.2 | 750 | 6 | CB823924 | CB823924 | EST 5148 |
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| c1022 | 50.8 | 2.2 | 896 | 8 | BZ652248 | BZ652248 | OGCBT21TM |
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| 1027 | 50.6 | 2.2 | 539 | 7 | CK893654 | CK893654 | SGP153746 |
| c1028 | 50.6 | 2.2 | 564 | 4 | BJ595115 | BJ595115 | BJ595115 |
| 1029 | 50.6 | 2.2 | 754 | 5 | BQ752889 | BQ752889 | WHE4120_D |
| 1030 | 50.6 | 2.2 | 769 | 9 | CE543749 | CE543749 | tigr-gss- |
| 1031 | 50.6 | 2.2 | 784 | 9 | CG103720 | CG103720 | PUFQS48TD |
| c1032 | 50.6 | 2.2 | 828 | 6 | CB621476 | CB621476 | OSIIEa07G |
| c1033 | 50.6 | 2.2 | 909 | 7 | CO235179 | CO235179 | WS0263.B2 |
| 1034 | 50.6 | 2.2 | 1758 | 9 | CL977417 | CL977417 | OsIFCC030 |

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| 1035 | 50.4 | 2.2 | 404 | 4 | BG730140 | BG730140 | de10c06.y |
| c1036 | 50.4 | 2.2 | 461 | 1 | AI527401 | AI527401 | uj46c05.x |
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| c1039 | 50.4 | 2.2 | 494 | 6 | CA403476 | CA403476 | EL01N0502 |
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| c1041 | 50.4 | 2.2 | 590 | 9 | CL190425 | CL190425 | 104_408_1 |
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| 1044 | 50.4 | 2.2 | 629 | 7 | CV095362 | CV095362 | FAMU_USDA |
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| c1051 | 50.4 | 2.2 | 700 | 9 | CL185025 | CL185025 | 104_398_1 |
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| 1057 | 50.4 | 2.2 | 1536 | 9 | CL949054 | CL949054 | OsIFSB003 |
| 1058 | 50.2 | 2.2 | 476 | 6 | CA117818 | CA117818 | SCBGLR104 |
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| 1063 | 50.2 | 2.2 | 583 | 7 | CR529808 | CR529808 | CR529808 |
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| c1065 | 50.2 | 2.2 | 665 | 4 | BJ275225 | BJ275225 | BJ275225 |
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| c1067 | 50.2 | 2.2 | 680 | 6 | CB680895 | CB680895 | OSJNEf06G |
| 1068 | 50.2 | 2.2 | 688 | 2 | BE403580 | BE403580 | WHE0434_C |
| c1069 | 50.2 | 2.2 | 696 | 7 | CR529807 | CR529807 | CR529807 |
| c1070 | 50.2 | 2.2 | 736 | 6 | CB650859 | CB650859 | OSJNEb15I |
| c1071 | 50.2 | 2.2 | 736 | 9 | CW516566 | CW516566 | OP_Ba004 |
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| c1074 | 50.2 | 2.2 | 755 | 6 | CB643719 | CB643719 | OSJNEb04J |
| c1075 | 50.2 | 2.2 | 755 | 6 | CB643721 | CB643721 | OSJNEb04J |
| c1076 | 50.2 | 2.2 | 765 | 6 | CB651523 | CB651523 | OSJNEb16I |
| c1077 | 50.2 | 2.2 | 771 | 6 | CB668190 | CB668190 | OSJNEd15O |
| c1078 | 50.2 | 2.2 | 778 | 6 | CB643291 | CB643291 | OSJNEb03O |
| c1079 | 50.2 | 2.2 | 785 | 6 | CB657829 | CB657829 | OSJNEc13H |
| c1080 | 50.2 | 2.2 | 800 | 6 | CB643653 | CB643653 | OSJNEb04H |
| 1081 | 50.2 | 2.2 | 811 | 6 | CB657828 | CB657828 | OSJNEc13H |
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| c1085 | 50 | 2.2 | 718 | 4 | BJ295169 | BJ295169 | BJ295169 |
| c1086 | 50 | 2.2 | 755 | 7 | CO119232 | CO119232 | GR_Eb022 |
| c1087 | 50 | 2.2 | 767 | 7 | CO117573 | CO117573 | GR_Eb01H |
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| 1091 | 49.8 | 2.1 | 401 | 4 | BI610047 | BI610047 | RH14915.5 |

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| 1096 | 49.8 | 2.1 | 552 | 7 | CF427347 |
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| 1106 | 49.8 | 2.1 | 706 | 7 | CN145147 |
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| 1146 | 49.4 | 2.1 | 793 | 7 | CO112194 |
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| CN149641 | WOUND1_64 |
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| CL187943 | 104_404_1 |
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| CO078974 | GR_Ea41I |
| CG213425 | OGXCM76TH |
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| CO364666 | RTK1_21_C |
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| CO119668 | GR_Eb022 |
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| CG369437 | OGYAP21TH |
| CG369451 | OGYAP21TV |
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| CB619200 | OSIIEa03J |
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| CG351341 | OGXAK06TH |
| BB743553 | BB743553 |

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| 1149 | 49.2 | 2.1 | 670 | 1 | AJ774738 | AJ774738 | AJ774738 |
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| c1152 | 49.2 | 2.1 | 752 | 6 | CB661740 | CB661740 | OSJNEd05A |
| 1153 | 49.2 | 2.1 | 764 | 9 | BX989346 | BX989346 | Reverse s |
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| 1156 | 49.2 | 2.1 | 826 | 9 | CG318335 | CG318335 | OG0FG24TH |
| c1157 | 49.2 | 2.1 | 850 | 9 | CG318346 | CG318346 | OG0FG24TV |
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| c1161 | 49.2 | 2.1 | 923 | 9 | CC726252 | CC726252 | OGUGI94TV |
| 1162 | 49.2 | 2.1 | 934 | 1 | AI064363 | AI064363 | GH04745.5 |
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| 1164 | 49 | 2.1 | 372 | 2 | BE425760 | BE425760 | WHE0316_C |
| 1165 | 49 | 2.1 | 505 | 7 | CO266931 | CO266931 | EK147954. |
| c1166 | 49 | 2.1 | 550 | 1 | AU246308 | AU246308 | AU246308 |
| 1167 | 49 | 2.1 | 655 | 6 | CB970156 | CB970156 | CAB10003_ |
| 1168 | 49 | 2.1 | 676 | 4 | BJ071376 | BJ071376 | BJ071376 |
| c1169 | 49 | 2.1 | 760 | 6 | CB620857 | CB620857 | OSIIEa06F |
| c1170 | 49 | 2.1 | 768 | 6 | CB970233 | CB970233 | CAB10003_ |
| 1171 | 49 | 2.1 | 866 | 6 | CA481981 | CA481981 | AGENCOURT |
| 1172 | 49 | 2.1 | 874 | 8 | CC113815 | CC113815 | NDL.34M4. |
| c1173 | 48.8 | 2.1 | 413 | 7 | CF649328 | CF649328 | 3530_1_68 |
| 1174 | 48.8 | 2.1 | 456 | 8 | BZ534563 | BZ534563 | OGALJ03TM |
| c1175 | 48.8 | 2.1 | 539 | 8 | BZ534560 | BZ534560 | OGALJ03TC |
| 1176 | 48.8 | 2.1 | 570 | 5 | BP274123 | BP274123 | BP274123 |
| 1177 | 48.8 | 2.1 | 601 | 7 | CV511561 | CV511561 | kc43h09.y |
| c1178 | 48.8 | 2.1 | 610 | 5 | BX559661 | BX559661 | BX559661 |
| c1179 | 48.8 | 2.1 | 645 | 9 | CC608615 | CC608615 | OGUAR12TV |
| 1180 | 48.8 | 2.1 | 723 | 7 | CO363008 | CO363008 | RTK1_7_C0 |
| 1181 | 48.8 | 2.1 | 734 | 7 | CV031446 | CV031446 | RTNACL1_1 |
| 1182 | 48.8 | 2.1 | 740 | 9 | CC608604 | CC608604 | OGUAR12TH |
| c1183 | 48.8 | 2.1 | 788 | 9 | CC647080 | CC647080 | OGNAF05TH |
| c1184 | 48.8 | 2.1 | 804 | 7 | CO526636 | CO526636 | 3530_1_17 |
| c1185 | 48.8 | 2.1 | 805 | 8 | BZ642226 | BZ642226 | OGAPA15TM |
| c1186 | 48.8 | 2.1 | 828 | 7 | CO367803 | CO367803 | RTK1_36_E |
| c1187 | 48.8 | 2.1 | 862 | 9 | CC660737 | CC660737 | OGLBT68TH |
| c1188 | 48.8 | 2.1 | 904 | 8 | CC326984 | CC326984 | OGIAX93TV |
| 1189 | 48.6 | 2.1 | 393 | 9 | CL948532 | CL948532 | OsIFSB005 |
| 1190 | 48.6 | 2.1 | 527 | 4 | BG052249 | BG052249 | RHIZ2_12_ |
| c1191 | 48.6 | 2.1 | 532 | 5 | BQ662175 | BQ662175 | HR01004u |
| 1192 | 48.6 | 2.1 | 654 | 6 | CA258723 | CA258723 | SCBGRT301 |
| c1193 | 48.6 | 2.1 | 685 | 7 | CF179609 | CF179609 | 814592 MA |
| c1194 | 48.6 | 2.1 | 770 | 7 | CR279298 | CR279298 | CR279298 |
| 1195 | 48.6 | 2.1 | 782 | 2 | BF256192 | BF256192 | HVSMEf000 |
| 1196 | 48.6 | 2.1 | 883 | 7 | CN019919 | CN019919 | AGENCOURT |
| 1197 | 48.4 | 2.1 | 339 | 7 | L33533 | L33533 | BNAESTF166 |
| c1198 | 48.4 | 2.1 | 396 | 5 | BQ540829 | BQ540829 | ps73a11.y |
| c1199 | 48.4 | 2.1 | 566 | 7 | CF630060 | CF630060 | zmrws48_0 |
| 1200 | 48.4 | 2.1 | 579 | 9 | CG118934 | CG118934 | PUIKV67TD |
| c1201 | 48.4 | 2.1 | 627 | 7 | CO518792 | CO518792 | 3530_1_12 |
| c1202 | 48.4 | 2.1 | 631 | 1 | AI711635 | AI711635 | 605058E04 |
| c1203 | 48.4 | 2.1 | 631 | 7 | CO518008 | CO518008 | 3530_1_11 |
| c1204 | 48.4 | 2.1 | 638 | 6 | CD721212 | CD721212 | VVB180H10 |
| c1205 | 48.4 | 2.1 | 639 | 6 | CD719709 | CD719709 | VVB164B11 |

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| c1206 | 48.4 | 2.1 | 644 | 6 | CD719870 | CD719870 | VVB166A11 |
| c1207 | 48.4 | 2.1 | 663 | 7 | CF630588 | CF630588 | zmrws48_0 |
| c1208 | 48.4 | 2.1 | 673 | 6 | CD406404 | CD406404 | Gm_ck3123 |
| c1209 | 48.4 | 2.1 | 675 | 7 | CO521120 | CO521120 | 3530_1_13 |
| c1210 | 48.4 | 2.1 | 681 | 6 | CD007604 | CD007604 | VVB073C12 |
| c1211 | 48.4 | 2.1 | 681 | 6 | CD713102 | CD713102 | VVB186C04 |
| c1212 | 48.4 | 2.1 | 683 | 6 | CD011026 | CD011026 | VVB118D02 |
| c1213 | 48.4 | 2.1 | 687 | 6 | CA202090 | CA202090 | SCSBFL104 |
| c1214 | 48.4 | 2.1 | 715 | 4 | BI967364 | BI967364 | GM830001B |
| c1215 | 48.4 | 2.1 | 720 | 8 | BZ688359 | BZ688359 | OGDAD91TC |
| c1216 | 48.4 | 2.1 | 731 | 9 | CC607404 | CC607404 | OGUFB75TH |
| 1217 | 48.4 | 2.1 | 751 | 9 | CG306324 | CG306324 | OG0GP22TH |
| c1218 | 48.4 | 2.1 | 753 | 8 | BZ544993 | BZ544993 | OGAJC02TC |
| c1219 | 48.4 | 2.1 | 754 | 9 | CC691465 | CC691465 | OGWDL65TH |
| c1220 | 48.4 | 2.1 | 809 | 9 | CG298983 | CG298983 | OGYBC45TV |
| 1221 | 48.4 | 2.1 | 836 | 9 | CG211806 | CG211806 | OG0AC10TH |
| 1222 | 48.4 | 2.1 | 844 | 2 | BE055475 | BE055475 | GA_Ea003 |
| c1223 | 48.4 | 2.1 | 861 | 7 | CO238672 | CO238672 | WS00722.B |
| 1224 | 48.4 | 2.1 | 876 | 7 | CO070998 | CO070998 | GR_Ea28G |
| c1225 | 48.4 | 2.1 | 877 | 9 | CG240612 | CG240612 | OGWAM46TV |
| c1226 | 48.4 | 2.1 | 896 | 9 | CG211814 | CG211814 | OG0AC10TV |
| c1227 | 48.4 | 2.1 | 905 | 6 | CD436944 | CD436944 | EL01N0365 |
| 1228 | 48.4 | 2.1 | 1027 | 9 | CNS02KWD | AL202054 | Tetraodon |
| 1229 | 48.4 | 2.1 | 1101 | 9 | CNS00BJK | AL057258 | Drosophil |
| 1230 | 48.4 | 2.1 | 1204 | 3 | AY108318 | AY108318 | Zea mays |
| 1231 | 48.2 | 2.1 | 344 | 9 | CE594014 | CE594014 | tigr-gss- |
| c1232 | 48.2 | 2.1 | 459 | 7 | CN072090 | CN072090 | 1021025E0 |
| 1233 | 48.2 | 2.1 | 494 | 6 | CA255455 | CA255455 | SCEPFL417 |
| 1234 | 48.2 | 2.1 | 623 | 5 | BQ854360 | BQ854360 | QGB23A16. |
| c1235 | 48.2 | 2.1 | 640 | 5 | BQ408246 | BQ408246 | GA_Ed000 |
| 1236 | 48.2 | 2.1 | 640 | 7 | CF426997 | CF426997 | PH1_3_C05 |
| 1237 | 48.2 | 2.1 | 832 | 9 | CG344045 | CG344045 | OGYAM82TV |
| 1238 | 48.2 | 2.1 | 838 | 9 | CG051217 | CG051217 | PUIAX51TD |
| c1239 | 48.2 | 2.1 | 844 | 9 | CC619390 | CC619390 | OGUED54TV |
| 1240 | 48.2 | 2.1 | 846 | 9 | CC638581 | CC638581 | OGVBC68TH |
| c1241 | 48.2 | 2.1 | 940 | 9 | CC638593 | CC638593 | OGVBC68TV |
| 1242 | 48.2 | 2.1 | 1088 | 6 | CA275165 | CA275165 | SCBFS103 |
| 1243 | 48 | 2.1 | 385 | 2 | BE406114 | BE406114 | WHE0404_c |
| c1244 | 48 | 2.1 | 446 | 8 | AZ047464 | AZ047464 | nbeb0094M |
| c1245 | 48 | 2.1 | 471 | 8 | AQ866659 | AQ866659 | nbeb0028P |
| 1246 | 48 | 2.1 | 492 | 2 | BE357084 | BE357084 | DG1_146_G |
| c1247 | 48 | 2.1 | 601 | 7 | CN444082 | CN444082 | Mdfw2001b |
| 1248 | 48 | 2.1 | 609 | 9 | CE605792 | CE605792 | tigr-gss- |
| 1249 | 48 | 2.1 | 637 | 6 | CD229006 | CD229006 | CCC1_11_D |
| 1250 | 48 | 2.1 | 666 | 6 | CD204458 | CD204458 | HS1_8_D09 |
| c1251 | 48 | 2.1 | 672 | 9 | CL389659 | CL389659 | RPCI44_28 |
| c1252 | 48 | 2.1 | 677 | 8 | AZ131490 | AZ131490 | OSJNBb011 |
| 1253 | 48 | 2.1 | 692 | 7 | CF434115 | CF434115 | NIT1_32_A |
| c1254 | 48 | 2.1 | 728 | 7 | CV234524 | CV234524 | WS01215.B |
| c1255 | 48 | 2.1 | 769 | 6 | CD866162 | CD866162 | AZO2_102L |
| 1256 | 48 | 2.1 | 1560 | 9 | CL967117 | CL967117 | OsIFCC014 |
| c1257 | 47.8 | 2.1 | 524 | 7 | CO236941 | CO236941 | WS0071.B2 |
| 1258 | 47.8 | 2.1 | 534 | 8 | BZ530624 | BZ530624 | OGALL21TC |
| c1259 | 47.8 | 2.1 | 575 | 4 | BJ130201 | BJ130201 | BJ130201 |
| c1260 | 47.8 | 2.1 | 586 | 1 | AU217077 | AU217077 | AU217077 |
| c1261 | 47.8 | 2.1 | 619 | 4 | BJ140963 | BJ140963 | BJ140963 |
| c1262 | 47.8 | 2.1 | 635 | 4 | BJ136724 | BJ136724 | BJ136724 |

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| 1263 | 47.8 | 2.1 | 679 | 7 | CF387087 | CF387087 | RTDR1_10 |
| 1264 | 47.8 | 2.1 | 683 | 6 | CA285250 | CA285250 | SCEQSD107 |
| c1265 | 47.8 | 2.1 | 713 | 4 | BJ132415 | BJ132415 | BJ132415 |
| c1266 | 47.8 | 2.1 | 719 | 9 | CC612397 | CC612397 | OGUCA43TV |
| 1267 | 47.8 | 2.1 | 728 | 6 | CA265146 | CA265146 | SCRFR305 |
| c1268 | 47.8 | 2.1 | 729 | 6 | CB619164 | CB619164 | OSIIEa03I |
| 1269 | 47.8 | 2.1 | 732 | 7 | CF385981 | CF385981 | RTDR1_7_E |
| 1270 | 47.8 | 2.1 | 801 | 7 | CF667004 | CF667004 | RTCNT1_27 |
| 1271 | 47.8 | 2.1 | 814 | 9 | CG208272 | CG208272 | OGWGN76TH |
| 1272 | 47.8 | 2.1 | 820 | 7 | CO172600 | CO172600 | NDL1_30_E |
| c1273 | 47.8 | 2.1 | 826 | 8 | BZ530629 | BZ530629 | OGALL21TM |
| c1274 | 47.8 | 2.1 | 833 | 8 | BZ643693 | BZ643693 | OGCCE77TC |
| c1275 | 47.8 | 2.1 | 834 | 7 | CV033205 | CV033205 | RTNACL1_3 |
| 1276 | 47.8 | 2.1 | 862 | 9 | CG235352 | CG235352 | OGWIR47TV |
| 1277 | 47.8 | 2.1 | 897 | 9 | CG170061 | CG170061 | PUIGK25TB |
| c1278 | 47.8 | 2.1 | 912 | 9 | CG208280 | CG208280 | OGWGN76TV |
| 1279 | 47.8 | 2.1 | 939 | 9 | CG308245 | CG308245 | OGVEF29TV |
| 1280 | 47.8 | 2.1 | 972 | 9 | CC630422 | CC630422 | OGLBS29TV |
| c1281 | 47.8 | 2.1 | 1101 | 9 | CNS000D1 | AL065414 | Drosophil |
| 1282 | 47.8 | 2.1 | 1458 | 9 | CL973238 | CL973238 | OsIFCC042 |
| 1283 | 47.8 | 2.1 | 1476 | 9 | CL959864 | CL959864 | OsIFCC036 |
| c1284 | 47.6 | 2.1 | 574 | 7 | CK095578 | CK095578 | UA14CPH12 |
| c1285 | 47.6 | 2.1 | 615 | 6 | CB872218 | CB872218 | HC07A12y |
| 1286 | 47.6 | 2.1 | 644 | 6 | CD235990 | CD235990 | SS1_25_B0 |
| c1287 | 47.6 | 2.1 | 674 | 9 | CL169524 | CL169524 | 104_368_1 |
| 1288 | 47.6 | 2.1 | 674 | 9 | CL192577 | CL192577 | 104_415_1 |
| 1289 | 47.6 | 2.1 | 704 | 7 | CF473082 | CF473082 | RTDS1_1_H |
| c1290 | 47.6 | 2.1 | 706 | 4 | BI968444 | BI968444 | GM830005A |
| c1291 | 47.6 | 2.1 | 717 | 4 | BJ284242 | BJ284242 | BJ284242 |
| 1292 | 47.6 | 2.1 | 870 | 9 | CL977898 | CL977898 | OsIFCC044 |
| c1293 | 47.6 | 2.1 | 910 | 7 | CV243458 | CV243458 | WS02518.B |
| 1294 | 47.4 | 2.0 | 367 | 1 | AV693675 | AV693675 | AV693675 |
| 1295 | 47.4 | 2.0 | 367 | 1 | AV694797 | AV694797 | AV694797 |
| 1296 | 47.4 | 2.0 | 367 | 1 | AV696603 | AV696603 | AV696603 |
| 1297 | 47.4 | 2.0 | 367 | 1 | AV696605 | AV696605 | AV696605 |
| 1298 | 47.4 | 2.0 | 367 | 1 | AV697866 | AV697866 | AV697866 |
| 1299 | 47.4 | 2.0 | 367 | 1 | AV698780 | AV698780 | AV698780 |
| 1300 | 47.4 | 2.0 | 367 | 1 | AV698800 | AV698800 | AV698800 |
| c1301 | 47.4 | 2.0 | 452 | 6 | CB684060 | CB684060 | OSJNef13D |
| c1302 | 47.4 | 2.0 | 536 | 6 | CB394655 | CB394655 | OSTR141F1 |
| 1303 | 47.4 | 2.0 | 556 | 2 | BF080514 | BF080514 | 231438_MA |
| c1304 | 47.4 | 2.0 | 592 | 6 | CA134676 | CA134676 | SCJFRT106 |
| c1305 | 47.4 | 2.0 | 694 | 6 | CB664715 | CB664715 | OSJNEd10J |
| c1306 | 47.4 | 2.0 | 753 | 6 | CB684061 | CB684061 | OSJNef13D |
| c1307 | 47.4 | 2.0 | 820 | 9 | CC604209 | CC604209 | OGUEL94TH |
| c1308 | 47.4 | 2.0 | 905 | 9 | CG308237 | CG308237 | OGVEF29TH |
| 1309 | 47.4 | 2.0 | 1473 | 9 | CL973231 | CL973231 | OsIFCC042 |
| c1310 | 47.2 | 2.0 | 396 | 8 | AQ843589 | AQ843589 | nbxb0024I |
| c1311 | 47.2 | 2.0 | 445 | 8 | AQ868140 | AQ868140 | nbeb0021H |
| 1312 | 47.2 | 2.0 | 585 | 5 | BQ702373 | BQ702373 | NXSI_127 |
| 1313 | 47.2 | 2.0 | 634 | 7 | CF471631 | CF471631 | RTDS1_4_B |
| 1314 | 47.2 | 2.0 | 641 | 7 | CF471539 | CF471539 | RTDS1_4_B |
| c1315 | 47.2 | 2.0 | 661 | 1 | AI402259 | AI402259 | GH11333.3 |
| 1316 | 47.2 | 2.0 | 681 | 7 | CN127822 | CN127822 | RHOH1_25 |
| c1317 | 47.2 | 2.0 | 692 | 7 | CF397219 | CF397219 | RTDS3_2_G |
| 1318 | 47.2 | 2.0 | 723 | 7 | CF478552 | CF478552 | RTWW3_20 |
| 1319 | 47.2 | 2.0 | 787 | 9 | CG210062 | CG210062 | OGWGK05TH |

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| c1320 | 47.2 | 2.0 | 800 | 6 | CB971452 | CB971452 | CAB10005 |
| .1321 | 47.2 | 2.0 | 801 | 7 | CK130111 | CK130111 | AGENCOURT |
| c1322 | 47.2 | 2.0 | 905 | 9 | CG210073 | CG210073 | OGWGK05TV |
| 1323 | 47.2 | 2.0 | 1092 | 9 | CNS020K7 | AL175696 | Tetraodon |
| 1324 | 47.2 | 2.0 | 1101 | 9 | CNS0039G | AL063921 | Drosophil |
| c1325 | 47 | 2.0 | 216 | 6 | CD944291 | CD944291 | RDF_6 Gen |
| 1326 | 47 | 2.0 | 216 | 6 | CD946848 | CD946848 | RET_82 Ge |
| c1327 | 47 | 2.0 | 216 | 6 | CD959938 | CD959938 | SCZ_156 G |
| 1328 | 47 | 2.0 | 216 | 6 | CF064465 | CF064465 | SeqID_63 |
| 1329 | 47 | 2.0 | 388 | 5 | BX283268 | BX283268 | BX283268 |
| 1330 | 47 | 2.0 | 447 | 1 | AA822117 | AA822117 | vp25h12.r |
| 1331 | 47 | 2.0 | 489 | 9 | CL973113 | CL973113 | OsIFCC042 |
| 1332 | 47 | 2.0 | 570 | 7 | CO529692 | CO529692 | 3530_1_19 |
| c1333 | 47 | 2.0 | 581 | 5 | BQ535603 | BQ535603 | STEM2_16 |
| c1334 | 47 | 2.0 | 588 | 4 | BI983739 | BI983739 | fu05h10.x |
| c1335 | 47 | 2.0 | 598 | 1 | AI964683 | AI964683 | 603021F04 |
| c1336 | 47 | 2.0 | 598 | 6 | CD453448 | CD453448 | WHE0752_C |
| 1337 | 47 | 2.0 | 610 | 7 | CF638057 | CF638057 | zmrww00_0 |
| 1338 | 47 | 2.0 | 660 | 6 | CB953865 | CB953865 | AGENCOURT |
| 1339 | 47 | 2.0 | 664 | 2 | BF787075 | BF787075 | 602108610 |
| 1340 | 47 | 2.0 | 664 | 6 | CA256133 | CA256133 | SCJLFL418 |
| 1341 | 47 | 2.0 | 731 | 6 | CA137836 | CA137836 | SCCART200 |
| c1342 | 47 | 2.0 | 776 | 9 | CG949887 | CG949887 | MBEGH16TF |
| c1343 | 47 | 2.0 | 782 | 7 | CK091254 | CK091254 | F066P42.3 |
| 1344 | 47 | 2.0 | 820 | 9 | CG322167 | CG322167 | OG3AP40TV |
| c1345 | 47 | 2.0 | 882 | 9 | CG322158 | CG322158 | OG3AP40TH |
| c1346 | 47 | 2.0 | 896 | 9 | CG455252 | CG455252 | PUFXJ44TB |
| c1347 | 47 | 2.0 | 981 | 9 | CG297863 | CG297863 | OG5CX89TC |
| 1348 | 46.8 | 2.0 | 327 | 2 | BE355206 | BE355206 | DG1_10_G0 |
| 1349 | 46.8 | 2.0 | 387 | 4 | BM158616 | BM158616 | NXLV_036 |
| 1350 | 46.8 | 2.0 | 429 | 2 | BE355032 | BE355032 | DG1_10_A0 |
| c1351 | 46.8 | 2.0 | 446 | 9 | CL585002 | CL585002 | OB_Ba007 |
| c1352 | 46.8 | 2.0 | 504 | 9 | CL166250 | CL166250 | 104_362_1 |
| 1353 | 46.8 | 2.0 | 515 | 6 | CA733021 | CA733021 | wlp1c.pk0 |
| c1354 | 46.8 | 2.0 | 537 | 6 | CB394617 | CB394617 | OSTR140G4 |
| 1355 | 46.8 | 2.0 | 556 | 7 | CF393594 | CF393594 | RTDR3_15 |
| 1356 | 46.8 | 2.0 | 569 | 7 | CF429042 | CF429042 | PH1_19_F0 |
| 1357 | 46.8 | 2.0 | 575 | 5 | BU100894 | BU100894 | WHE3359_B |
| 1358 | 46.8 | 2.0 | 578 | 4 | BJ521530 | BJ521530 | BJ521530 |
| c1359 | 46.8 | 2.0 | 590 | 6 | CD289695 | CD289695 | StrPu691. |
| 1360 | 46.8 | 2.0 | 597 | 2 | BE593270 | BE593270 | WS1_99_F1 |
| c1361 | 46.8 | 2.0 | 619 | 4 | BJ239537 | BJ239537 | BJ239537 |
| c1362 | 46.8 | 2.0 | 629 | 7 | CO083786 | CO083786 | GR_Ea49A |
| c1363 | 46.8 | 2.0 | 697 | 1 | AU210371 | AU210371 | AU210371 |
| c1364 | 46.8 | 2.0 | 714 | 6 | CA398399 | CA398399 | EL01N0303 |
| c1365 | 46.8 | 2.0 | 720 | 7 | CO112193 | CO112193 | GR_Eb004 |
| 1366 | 46.8 | 2.0 | 752 | 7 | CN142613 | CN142613 | WOUND1_11 |
| 1367 | 46.8 | 2.0 | 758 | 7 | CF666932 | CF666932 | RTCNT1_27 |
| 1368 | 46.8 | 2.0 | 778 | 7 | CF393653 | CF393653 | RTDR3_15 |
| c1369 | 46.8 | 2.0 | 807 | 9 | CG317189 | CG317189 | OGXDU28TH |
| c1370 | 46.8 | 2.0 | 865 | 9 | CG350507 | CG350507 | OG3AM53TV |
| 1371 | 46.8 | 2.0 | 908 | 7 | CO645622 | CO645622 | ILLUMIGEN |
| 1372 | 46.8 | 2.0 | 936 | 7 | CN324479 | CN324479 | AGENCOURT |
| 1373 | 46.6 | 2.0 | 409 | 4 | BG241163 | BG241163 | OV1_39_A0 |
| 1374 | 46.6 | 2.0 | 566 | 2 | BF789422 | BF789422 | 602103472 |
| 1375 | 46.6 | 2.0 | 584 | 2 | BE364586 | BE364586 | PI1_15_G0 |
| 1376 | 46.6 | 2.0 | 601 | 2 | BF785829 | BF785829 | 602112453 |

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|-------|------|-----|------|---|-----------|----------|------------|
| 1377 | 46.6 | 2.0 | 606 | 5 | BX628417 | BX628417 | BX628417 |
| c1378 | 46.6 | 2.0 | 609 | 1 | AI790589 | AI790589 | ul03h02.x |
| 1379 | 46.6 | 2.0 | 627 | 5 | BQ864555 | BQ864555 | QGC27A13. |
| 1380 | 46.6 | 2.0 | 635 | 5 | BU692265 | BU692265 | JM01037H1 |
| c1381 | 46.6 | 2.0 | 649 | 7 | CV523852 | CV523852 | Mdlv2_401 |
| 1382 | 46.6 | 2.0 | 672 | 7 | CF403057 | CF403057 | RTWW1_24_ |
| 1383 | 46.6 | 2.0 | 680 | 7 | CF402964 | CF402964 | RTWW1_24_ |
| 1384 | 46.6 | 2.0 | 694 | 4 | BI507584 | BI507584 | BB170013B |
| c1385 | 46.6 | 2.0 | 700 | 6 | CD876252 | CD876252 | AZO3.109B |
| 1386 | 46.6 | 2.0 | 826 | 9 | CG312200 | CG312200 | OGWKS36TV |
| c1387 | 46.6 | 2.0 | 930 | 9 | CNS01367 | AL102457 | Drosophil |
| c1388 | 46.6 | 2.0 | 932 | 7 | CO214524 | CO214524 | WS00928.B |
| 1389 | 46.6 | 2.0 | 966 | 4 | BG430589 | BG430589 | 602502243 |
| 1390 | 46.6 | 2.0 | 1416 | 3 | AY110944 | AY110944 | Zea mays |
| c1391 | 46.4 | 2.0 | 226 | 9 | FR0014931 | AL006140 | F.rubripe |
| 1392 | 46.4 | 2.0 | 405 | 5 | BQ702864 | BQ702864 | NXSI_133_ |
| 1393 | 46.4 | 2.0 | 406 | 7 | CN445015 | CN445015 | Mdfw2001b |
| c1394 | 46.4 | 2.0 | 415 | 7 | CV235889 | CV235889 | WS01221.B |
| 1395 | 46.4 | 2.0 | 476 | 2 | BE358440 | BE358440 | DG1_29_G1 |
| c1396 | 46.4 | 2.0 | 486 | 8 | AQ860883 | AQ860883 | nbeb0015L |
| 1397 | 46.4 | 2.0 | 507 | 2 | BE940767 | BE940767 | 900014 Av |
| 1398 | 46.4 | 2.0 | 521 | 6 | CA615835 | CA615835 | wrl.pk169 |
| 1399 | 46.4 | 2.0 | 542 | 4 | BI801893 | BI801893 | H064C08 E |
| 1400 | 46.4 | 2.0 | 549 | 4 | BJ281677 | BJ281677 | BJ281677 |
| 1401 | 46.4 | 2.0 | 556 | 6 | CB259745 | CB259745 | 25-E9602- |
| c1402 | 46.4 | 2.0 | 564 | 7 | CV233345 | CV233345 | WS01210.B |
| c1403 | 46.4 | 2.0 | 579 | 1 | AV831789 | AV831789 | AV831789 |
| 1404 | 46.4 | 2.0 | 583 | 4 | BG410775 | BG410775 | EM1_25_F0 |
| c1405 | 46.4 | 2.0 | 601 | 7 | CV233333 | CV233333 | WS0121.B2 |
| 1406 | 46.4 | 2.0 | 604 | 5 | BU038781 | BU038781 | DH08c09 H |
| 1407 | 46.4 | 2.0 | 628 | 6 | CA076768 | CA076768 | SCMCAM110 |
| 1408 | 46.4 | 2.0 | 634 | 2 | BE405606 | BE405606 | WHE1209_C |
| 1409 | 46.4 | 2.0 | 656 | 5 | BQ743938 | BQ743938 | WHE4109_H |
| 1410 | 46.4 | 2.0 | 662 | 5 | BQ578302 | BQ578302 | WHE0301_D |
| c1411 | 46.4 | 2.0 | 680 | 6 | CD373574 | CD373574 | WHE0425_A |
| c1412 | 46.4 | 2.0 | 697 | 1 | AV784375 | AV784375 | AV784375 |
| 1413 | 46.4 | 2.0 | 723 | 6 | CD865781 | CD865781 | AZO2.101M |
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| 1416 | 46.4 | 2.0 | 817 | 7 | CN520132 | CN520132 | GQ0106.B3 |
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| c1418 | 46.4 | 2.0 | 848 | 7 | CV282585 | CV282585 | WS0185.B2 |
| c1419 | 46.4 | 2.0 | 883 | 7 | CV236193 | CV236193 | WS01223.B |
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| 1421 | 46.4 | 2.0 | 1447 | 3 | CNS0A460 | BX826605 | Arabidops |
| 1422 | 46.4 | 2.0 | 1523 | 3 | CNS0A40Y | BX827027 | Arabidops |
| 1423 | 46.2 | 2.0 | 164 | 7 | T69701 | T69701 | yc44h12.r1 |
| 1424 | 46.2 | 2.0 | 286 | 8 | BZ729579 | BZ729579 | OGEDD27TC |
| 1425 | 46.2 | 2.0 | 330 | 2 | BE187215 | BE187215 | NXNV_160_ |
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| 1430 | 46.2 | 2.0 | 532 | 8 | BZ716462 | BZ716462 | OGEBF10TM |
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| c1433 | 46.2 | 2.0 | 568 | 8 | AQ966294 | AQ966294 | LERIJ28TR |

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| c1439 | 46.2 | 2.0 | 651 | 1 | AV927784 | AV927784 | AV927784 |
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| 1441 | 46.2 | 2.0 | 658 | 5 | BQ405465 | BQ405465 | GA_Ed008 |
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| c1454 | 46 | 2.0 | 428 | 6 | CA930524 | CA930524 | MTU4CA.P2 |
| c1455 | 46 | 2.0 | 428 | 6 | CA930625 | CA930625 | MTU4CA.P2 |
| 1456 | 46 | 2.0 | 534 | 1 | AJ771629 | AJ771629 | AJ771629 |
| 1457 | 46 | 2.0 | 588 | 2 | BE213331 | BE213331 | EST0099 T |
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| 1460 | 46 | 2.0 | 664 | 6 | CD715895 | CD715895 | VVB218C02 |
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| c1471 | 45.8 | 2.0 | 608 | 2 | BE149486 | BE149486 | RC1-HT025 |
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| c1486 | 45.6 | 2.0 | 649 | 7 | CO238128 | CO238128 | WS0074.B2 |
| c1487 | 45.6 | 2.0 | 654 | 9 | CL147747 | CL147747 | 104_327_1 |
| 1488 | 45.6 | 2.0 | 687 | 2 | BB667752 | BB667752 | BB667752 |
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| 1494 | 45.6 | 2.0 | 769 | 7 | CF396075 | CF396075 | RTDS2_13_ |
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| c1496 | 45.6 | 2.0 | 802 | 4 | BJ786742 | BJ786742 | BJ786742 |
| 1497 | 45.6 | 2.0 | 817 | 7 | CN763120 | CN763120 | ID0AAA6AF |
| c1498 | 45.6 | 2.0 | 827 | 8 | BZ724654 | BZ724654 | OGFAB52TM |
| c1499 | 45.4 | 2.0 | 494 | 2 | BE186818 | BE186818 | 946012G11 |
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ALIGNMENTS

RESULT 1

AY404343

LOCUS AY404343 1182 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404343

VERSION AY404343.1 GI:39760320

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1182)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1182)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..1182

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

gene <1..>1182

/locus_tag="HCM1859"

ORIGIN

Query Match 50.9%; Score 1180.4; DB 9; Length 1182;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2

AK050128

LOCUS AK050128 2197 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730018P11 product:hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK050128

VERSION AK050128.1 GI:26340835

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2197)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2197 /organism="Mus musculus"

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ORIGIN

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Qy     241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
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Db     272 TGAAA---GTGCTAATATCCCAGATTTTAGAAAGGAAAAACCATCATATCAAGTTATTAA 328

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| | | | |
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| Qy | 301 | TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA | 360 |
| | | | |
| Db | 329 | TTGGCGTCCACCTGAAGATCAGGAAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA | 388 |
| Qy | 361 | AGAAACTTTAGGTGGCAGAGGAAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC | 420 |
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| Db | 389 | AGAAATAACTTATGGCAGGTCCAAACATCACACCCTTCTAAAGATCCATCAATACTTTGG | 448 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA | 480 |
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| Db | 449 | GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA | 508 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
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| Db | 509 | CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT | 568 |
| Qy | 541 | TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC | 600 |
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| Db | 569 | TGGGAAACGATTTGTGTCTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGTTACC | 628 |
| Qy | 601 | AA---TCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTT | 657 |
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| Db | 629 | AAGCGCCCCCTGTCCATGCTCCAGTGTATGGTCTGGTCTAACTGACCAAATGGACTT | 688 |
| Qy | 658 | CTGGGGCCGAGTGAAGAAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT | 717 |
| | | | |
| Db | 689 | CTGGGGCCGAGTGAAGAACTTTCTGATGTTCTTTGATTTCTCCATGAAGCAAAGGGAAAT | 748 |
| Qy | 718 | GCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTT | 777 |
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| Db | 749 | CCTTTCCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT | 808 |
| Qy | 778 | GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT | 837 |
| | | | |
| Db | 809 | GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT | 868 |
| Qy | 838 | TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA | 897 |
| | | | |
| Db | 869 | TGCTCGTCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTGGACAAACCTGTTCA | 928 |
| Qy | 898 | ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCT | 957 |
| | | | |
| Db | 929 | GCCAATACCCAAGACTTGGAGAAATTTATCTCTCAGTTTGGAGACTCAGGTTTTGTCT | 988 |
| Qy | 958 | TGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAA | 1017 |
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| Db | 989 | TGTGGCCCTGGGCTCTATAGTGAGCATGATTCAAGTCCAAGGAAATTTAAGGAGATGAA | 1048 |
| Qy | 1018 | CAATGCCTTTGCTCACCTACCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCC | 1077 |
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| Db | 1049 | CAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAGACTTCTCATTGGCC | 1108 |
| Qy | 1078 | CAAAGATGTCCACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCCCTCAGAGTGACCT | 1137 |
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| Db | 1109 | CAAAGATGTGAGTTTGGCCCCAAATGTCAAATCATGGATTGGCTTCCACAGACTGACCT | 1168 |

Qy 1138 CCTGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGA 1197
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 Db 1169 TCTAGCTCACCTAGCATTTCGTCTGTTTGTCACTCATGGAGGGATGAACAGTGTGATGGA 1228

Qy 1198 GGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAA 1257
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 Db 1229 GGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCATTTTTTTTTTGACCAACCTGAAAA 1288

Qy 1258 CATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTTCAGTTAAAGAAGCTCAAGGC 1317
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 Db 1289 CATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTATTTCAGCTACAGACGCTCAAGGC 1348

Qy 1318 AGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGC 1377
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 Db 1349 AGAGTCATTTGCGCTCACCATGAAAAAATCATAGAAGACAAGAGGTACAAGTCTGCAGC 1408

Qy 1378 AGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGG 1437
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 Db 1409 AATGGCCTCCAAGATTATCAGGCACTCCCACCCACTGACCCCTGCCAGAGGCTTTTGGG 1468

Qy 1438 CTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCA 1497
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 Db 1469 CTGGATAGATCATATCTTGCAGACAGGGGGTGCAGCACATCTCAAGCCATATGCTTTCCA 1528

Qy 1498 GCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCT 1557
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 Db 1529 GCAGCCATGGCATGAGCAGTACATGCTTGATGTCTTCCTCTTCTCCTAGGGCTCATGCT 1588

Qy 1558 GGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGC 1617
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 Db 1589 GGGTACTTTGTGGCTTAGTGTAAGGTTCTTGTTGCTGTAACCAGGTATCTGAGTATAGC 1648

Qy 1618 CAGAAAGGTGAAGGAGACATAAGGC 1642
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 Db 1649 AACGAAGGTCAAGGAGGCATAATGC 1673

RESULT 3

AY404344

LOCUS AY404344 1180 bp DNA linear GSS 12-DEC-2003

DEFINITION Pan troglodytes HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. -

ACCESSION AY404344

VERSION AY404344.1 GI:39760321

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee).

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1180)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302
REFERENCE 2 (bases 1 to 1180)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1. .1180
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1..>1180
/locus_tag="HCM1859"

ORIGIN

Query Match 37.0%; Score 857.4; DB 9; Length 1180;
Best Local Similarity 73.0%; Pred. No. 8.5e-232;
Matches 861; Conservative 0; Mismatches 319; Indels 0; Gaps 0;

Qy 460 GGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCC 519
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Db 1 GGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCC 60

Qy 520 TTTCCTGATTGCTGAGAAGCTTGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGG 579
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Db 61 TTTCCTGATTGCTGAGAAGCTTGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGG 120

Qy 580 CTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCT 639
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Db 121 CTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCT 180

Qy 640 GACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTG 699
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Db 181 GACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTG 240

Qy 700 CAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGA 759
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Db 241 CAGGAGGCAATGGGACATGCAGTCTACATTTGACAACACCATCAAGGAGCATTTCCCAGA 300

Qy 760 AGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC TC 819
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Db 301 AGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTNNNTTAACTC 360

Qy 820 TGA CTTTGCCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTT 879
|| |||||
Db 361 TGNNNTTGCCTTTGATTTTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 420

Qy 880 GATGGA AAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGG 939
Db 421 NNN 480

Qy 940 GGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGA 999

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 879)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13284 row: 1 column: 23
 High quality sequence start: 17
 High quality sequence stop: 671.

FEATURES Location/Qualifiers

source 1. .879
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6043558"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 36.8%; Score 853.2; DB 5; Length 879;
 Best Local Similarity 99.0%; Pred. No. 1.2e-230;
 Matches 869; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 780 CTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTG 839
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Db 1 CTCATCTTCTACTGAAAGCAGAGATGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTG 60

Qy 840 CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAAC 899
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Db 61 CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAAC 120

Qy 900 CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG 959
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Db 121 CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG 180

Qy 960 TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACA 1019
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Db 181 TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACA 240

Qy 1020 ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCA 1079
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Db 241 ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCA 300
 Qy 1080 AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC 1139
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC 360
 Qy 1140 TGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGG 1199
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 Db 361 TGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGG 420
 Qy 1200 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 1259
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 Db 421 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 480
 Qy 1260 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTAGTTAAAGAAGCTCAAGGCAG 1319
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 Db 481 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTAGTTAAAGAAGCTCAAGGCAG 540
 Qy 1320 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 1379
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 Db 541 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 600
 Qy 1380 TGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 1439
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 Db 601 TGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 660
 Qy 1440 GGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 1499
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 Db 661 GGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 720
 Qy 1500 AGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 1559
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 Db 721 AGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 780
 Qy 1560 GGACTCTATGGCTTTGT-GGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCC 1618
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 Db 781 GGACTCTATGGCTTTGTGGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCTTGGGGCC 840
 Qy 1619 AGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 1656
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 Db 841 ACAAAGGGGAAGGAGACCTAAAGCCAGGTGCACCCTTG 878

RESULT 5

CN396938

LOCUS CN396938 759 bp mRNA linear.. EST 16-MAY-2004

DEFINITION 17000417785787 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN396938

VERSION CN396938.1 GI:47384533

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 759)

AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,

Qy 421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
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 Db 426 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 485
 Qy 481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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 Db 486 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 545
 Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
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 Db 546 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 605
 Qy 601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 660
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 Db 606 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 665
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 Db 666 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 725
 Qy 721 GTCTACATTTGACAACACCATCAAGGAACATTTTC 754
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 Db 726 GTCTACATTTGACAACACCATCAAGGAACATTTTC 759

RESULT 6
 CD050395

LOCUS CD050395 916 bp mRNA linear EST 09-MAY-2003
 DEFINITION AGENCOURT_13977999 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CD050395
 VERSION CD050395.1 GI:30487290
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 916)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDKM37 row: m column: 04
 High quality sequence start: 12
 High quality sequence stop: 721.
 FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/tissue_type="embryonic trophoblasts, made from WA01 stem
cells"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_173"
/note="Vector: pDONR201; Site_1: attP2; Site_2: attP1;
LIBR PRIMING - oligo dT; METHOD - full-length enriched;
LIBR PROVIDER - Bradfield"

ORIGIN

Query Match 31.8%; Score 738; DB 6; Length 916;
Best Local Similarity 95.0%; Pred. No. 7.2e-198;
Matches 795; Conservative 0; Mismatches 36; Indels 6; Gaps 3;

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Db      54 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 113

Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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Db     114 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 173

Qy     121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Db     174 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 233

Qy     181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
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Db     234 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 293

Qy     241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300
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Db     294 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 353

Qy     301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA 360
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Db     354 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA 413

Qy     361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
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Db     414 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 473

Qy     421 GTTGCAGTGCAGTCATTTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
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Db     474 GTTGCAGTGCAGTCATTTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 533

Qy     481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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Db     534 CTTGACAT-GTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 592

Qy     541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACC 600
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Db     593 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACC 652

Qy     601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 660
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Db     653 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 712
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Qy 661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
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 Db 713 GGGCCGAGTGAAGAATTTTCTGATNGTCTTTAGTTTCTGCAGGAAGCAACAGCACATGCA 772

Qy 721 GTCTACATTTGACAACACCATCAAGGAACA--TTTCACAGAAGGCTCTAGGCCAGTTTTG 778
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 Db 773 GTCTACATTTGACAACACCATCCAAGGACATTTTTCACAGAGGGCTCTAGGGCCAGTTTT 832

Qy 779 TCTC---ATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTT 832
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 Db 833 GTCCTCAATCTTCTACTGAAAAGCAAAGTTGGTGGGTTCAATTAACCTCTGGACTT 889

RESULT 7

AY404345

LOCUS AY404345 1185 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404345

VERSION AY404345.1 GI:39760322

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers
 source 1..1185
 /organism="Mus musculus"
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 /db_xref="taxon:10090"
 gene <1..>1185
 /locus_tag="HCM1859"

ORIGIN

Query Match 31.6%; Score 733.8; DB 9; Length 1185;
 Best Local Similarity 76.8%; Pred. No. 1.3e-196;
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Qy 458 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAACTTTTGACTACTGT 517
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Qy 518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCACCTTCATTTC 577
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 Db 781 TTTTTTTTTGACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCT 840

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection .

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1353)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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CDS

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FVSFLPFQFSYMDLGLPSAPLSYAPVYGSGLTDQMDFWGRVKNFLMFLDFSMKQREIL
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ORIGIN

Query Match 31.5%; Score 731.6; DB 3; Length 1353;
 Best Local Similarity 73.1%; Pred. No. 5.6e-196;
 Matches 981; Conservative 0; Mismatches 354; Indels 7; Gaps 3;

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Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT 120
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Db      76 TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGAGGTTAT 135

Qy      121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Qy      181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
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Db      196 GATAAGCCGTGTGTGCGCAAGTTCTTCATGAAGGTGGCCACAATGTGACCAAACCTCTTTA 255

Qy      241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300
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Qy      361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
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 Db 1339

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| Qy | 764 | TCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGAC | 823 |
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| Qy | 824 | TTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATG | 883 |
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| | | 181 TTTGCCTTGGATTTTGTCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTG | 240 |
| Qy | 884 | GAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGAC | 943 |
| Db | 241 | | |
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| Qy | 944 | TCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATC | 1003 |
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| | | 361 ATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAG | 420 |
| Qy | 1064 | TGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTT | 1123 |
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| | | 541 AACAGTGTAATGGAGGCTGTCCATCATGGAGTACCAATGGTAGGGATTCCATTTTTTGA | 600 |
| Qy | 1244 | GACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTTCAGTTA | 1303 |
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| Db | 778 | ... | |
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RESULT 10

LOCUS

CN396939

510 bp

mRNA

linear

EST 16-

Y-2004

DEFINITION 17000599940872 GRN PRENEU Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN396939
 VERSION CN396939.1 GI:47384534
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 510)
 AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J and Stanton, L.W.
 TITLE Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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 conditions. Embryoid bodies were generated in the presence
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ORIGIN

Query Match 21.8%; Score 506.4; DB 7; Length 510;
 Best Local Similarity 99.8%; Pred. No. 4.5e-132;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 183 GTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 242
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RESULT 11

CR769328

LOCUS CR769328 717 bp mRNA linear EST 23-SEP-2004

DEFINITION DKFZp469O0528_r1 469 (synonym: pkidl) Pongo pygmaeus cDNA clone
DKFZp469O0528 5', mRNA sequence.

ACCESSION CR769328

VERSION CR769328.1 GI:52613343

KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

REFERENCE 1 (bases 1 to 717)

AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

TITLE Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
Deutschenbaur,S., et al.)

JOURNAL Unpublished (2004)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix

(Martinsried/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp469O0528) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:

<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469O0528>

Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

Location/Qualifiers

1. .717

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

Db 664 GGAGCCCNATGGGGACATGCAGTCTACATTTGGACAACNCCNTCAAGGAGCATT 717

RESULT 12

BI559553

LOCUS BI559553 761 bp mRNA linear EST 05-SEP-2001

DEFINITION 603252894F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295502 5', mRNA sequence.

ACCESSION BI559553

VERSION BI559553.1 GI:15446867

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 761)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL).

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11747 row: k column: 23

High quality sequence stop: 726.

FEATURES Location/Qualifiers

source

1. .761

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/clone_lib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein

(NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.1%; Score 488.6; DB 4; Length 761;

Best Local Similarity 80.7%; Pred. No. 6.1e-127;

Matches 608; Conservative 0; Mismatches 139; Indels 6; Gaps 3;

QY 8 CTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAGC 67

| Db | 6 | CTTAGCCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAGC | 65 |
|----|-----|---|-----|
| Qy | 68 | ATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTCTCA | 127 |
| Db | 66 | ATGGTTGGGCAGCGGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCTGCTCTCA | 125 |
| Qy | 128 | GAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGAC | 187 |
| Db | 126 | GAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGAC | 185 |
| Qy | 188 | CGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCACAAAAGA | 247 |
| Db | 186 | CGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGGA | 245 |
| Qy | 248 | GGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTT | 307 |
| Db | 246 | AAGTTTGGATCCCAGATATTAAAGAGGAGGAAAATCATACCAAGTTATCAGGTGGTTT | 305 |
| Qy | 308 | GCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACT | 367 |
| Db | 306 | TCACCTGAAGATCATCAAAAAAGAATTAAGAAGCATTTTGATAGCTACATAGAAACAGCA | 365 |
| Qy | 368 | TTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAG | 427 |
| Db | 366 | TTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCAA | 425 |
| Qy | 428 | TGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGAC | 487 |
| Db | 426 | TGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCCTTAAAGAATGAGAACTATGAT | 485 |
| Qy | 488 | ATGGTGATAGTTGAA-ACCTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAA | 546 |
| Db | 486 | CTGGTATTTGTTGAACGCATTTGATTTCTGTTCTTTCCTGATTGCTGAGAAGCTTGTGAA | 545 |
| Qy | 547 | GCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCC | 606 |
| Db | 546 | ACCATTTGTGGCCATTCTTCCCACCACATTCGGCTCTATGGATTGTTGGGCTACCAAGCCC | 605 |
| Qy | 607 | CTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACT-GATCACATGGACTTCTGGGGCC | 665 |
| Db | 606 | CTTGTCTTATGTTCCAGTATTCCCTTCCCTTGCTGACTGGATCACATGGACTTCTGGGGCC | 665 |
| Qy | 666 | GAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGG----CAACAGCACATGCAG | 721 |
| Db | 666 | GAGTGAAGAAATTTCTGATGTCTTTAGTTTCTCCTCAAGGAGCCCAATGGGACATGCAG | 725 |
| Qy | 722 | TCTACATTTGACAACACCATCAAGGAACATTTT | 754 |
| Db | 726 | TCTACAATTTGACAACACATCAAGGAGCATTTT | 758 |

RESULT 13
AW173071/c

2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ;,
mRNA sequence.

ACCESSION AW173071

VERSION AW173071.1 GI:6439019

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 694)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 412.

FEATURES
source Location/Qualifiers
1. .694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2663780"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 20.0%; Score 463.6; DB 2; Length 694;
Best Local Similarity 83.5%; Pred. No. 7.7e-120;
Matches 537; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

Qy 268 TAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCATCAAAG 327
|| |||| | ||| || || |||| | || | |||||

Db 643 TATAAAGAGAAGCAAAATTCATACAGGTATCCGGGTGGTTTTTCACCTAAGATCATCAAAA 584

Qy 328 AGAATTTAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAATT 387
|||| |||| ||| ||||| || | ||| | ||||| |||

Db 583 AGAA-TTAAGAAGCATTTTGATAGCTACATAGAAACAGCATTGGATGGCAGAAAAGAATC 525

Qy 388 TGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAG 447
|||| | | || | | ||| || || | || |||| ||| ||

Db 524 TGAAGCCCTTGTANAGCTAATGGAAATATTTGGGACTCAATGTAGTTATTTGCTAAGCAG 465

Db 178 ATCACCAAATTTGGAGACTCTGGTTTTGTCCTTGTAAAGCCTGGGGTCCATGGTGAGTTTC 119

Qy 986 TGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGG 1045
 || | | || | |||| ||||| ||||| || || |||||

Db 118 ATTCGGTCCCAGGAGTTCTCAAAGAGATGAATGCTGCCTTTGCTCATCTCCCTCAAGGG 59

Qy 1046 GTGATATGGAAGTGTCTAGTGTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAA 1101
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Db 58 GTGATATGGAAGTATAATCCTTCTCATTGGCCCCAAAGACATCAAATTGGCCCCAAA 3

RESULT 15

AK052644

LOCUS AK052644 1723 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630011D02 product:hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK052644

VERSION AK052644.1 GI:26095303

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE

5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1723)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES

source Location/Qualifiers

1. .1723

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:D630011D02"

/db_xref="taxon:10090"

/clone="D630011D02"

/tissue_type="kidney"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="0 day neonate"

misc_feature

1. .1723

/note="hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein (InterPro|IPR002213, evidence: InterPro)"

ORIGIN

Query Match 19.5%; Score 452.6; DB 3; Length 1723;

Best Local Similarity 69.1%; Pred. No. 1.5e-116;

Matches 649; Conservative 0; Mismatches 284; Indels 6; Gaps 2;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

|||||

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| Db | 41 | AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTGTCAGGGCTCCACATAT | 100 |
| Qy | 61 | AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT | 120 |
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| Db | 101 | TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGAGGTTAT | 160 |
| Qy | 121 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 180 |
| | | | |
| Db | 161 | TCTCTTGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT | 220 |
| Qy | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 240 |
| | | | |
| Db | 221 | GATAAGCCGTGTGTCGCAAGTTCCTCATGAAGGTGGCCACAATGTGACCAAACCTCTTTA | 280 |
| Qy | 241 | CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG | 300 |
| | | | |
| Db | 281 | TGAAA---GTGCTAATATCCCAGATTTTAGAAAAGGAAAAACCATCATATCAAGTTATTAA | 337 |
| Qy | 301 | TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA | 360 |
| | | | |
| Db | 338 | TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA | 397 |
| Qy | 361 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC | 420 |
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| Db | 398 | AGAAATAACTTATGGCAGGTCCAAACATCACACCCTTCTAAAGATCCATCAATACTTTGG | 457 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA | 480 |
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| Db | 458 | GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA | 517 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTCTCTGATTGCTGAGAAGCT | 540 |
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| Db | 518 | CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT | 577 |
| Qy | 541 | TGGGAAGCCATTGTGCGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC | 600 |
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| Db | 578 | TGGGAAACGATTGTGTCTTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGTTACC | 637 |
| Qy | 601 | AA---TCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTT | 657 |
| | | | |
| Db | 638 | AAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTTCTGGTCTAACTGACCAAATGGACTT | 697 |
| Qy | 658 | CTGGGGCCGAGTGAAGAAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT | 717 |
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| Db | 698 | CTGGGGCCGAGTGAAGAACTTTCTGATGTTCTTGATTCTCCATGAAGCAAAGGGAAAT | 757 |
| Qy | 718 | GCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTT | 777 |
| | | | |
| Db | 758 | CCTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT | 817 |
| Qy | 778 | GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT | 837 |
| | | | |
| Db | 818 | GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT | 877 |
| Qy | 838 | TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA | 897 |
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| Db | 878 | TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTGGACAAACCTGTTCA | 937 |

Qy 898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTT 936
||| |||| |||| || || || | || ||
Db 938 GCCAATACCCCAAGTAAGTGACAAATTAGCTCTCACTTT 976

Search completed: February 15, 2005, 09:44:23
Job time : 6858 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:26:17 ; Search time 9715 Seconds
(without alignments)
11571.395 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccggg'gc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | % | | | | | Description |
|--------|--------|-------|--------|----|----------|--|--------------------|
| Result | Query | Match | Length | DB | ID | | |
| No. | Score | | | | | | |
| 1 | 2320 | 100.0 | 2320 | 6 | AX697213 | | AX697213 Sequence |
| 2 | 2320 | 100.0 | 2320 | 9 | AY358416 | | AY358416 Homo sapi |
| 3 | 2310.2 | 99.6 | 2341 | 6 | AX136141 | | AX136141 Sequence |

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|---|----|--------|------|--------|----|------------|----------|-------------|
| | 4 | 2310.2 | 99.6 | 2341 | 6 | BD123523 | BD123523 | Secretary |
| | 5 | 2310.2 | 99.6 | 2341 | 9 | AK075383 | AK075383 | Homo sapi |
| | 6 | 2102.8 | 90.6 | 2944 | 6 | AX548037 | AX548037 | Sequence |
| | 7 | 1578.8 | 68.1 | 2263 | 6 | AX958403 | AX958403 | Sequence |
| | 8 | 1281.6 | 55.2 | 2082 | 6 | AX359921 | AX359921 | Sequence |
| | 9 | 1281.6 | 55.2 | 2797 | 6 | AX155211 | AX155211 | Sequence |
| | 10 | 1281.6 | 55.2 | 2823 | 6 | AX714604 | AX714604 | Sequence |
| | 11 | 1281.6 | 55.2 | 2823 | 9 | AK057066 | AK057066 | Homo sapi |
| | 12 | 1280.6 | 55.2 | 2759 | 9 | BC068446 | BC068446 | Homo sapi |
| | 13 | 1280 | 55.2 | 2086 | 6 | AX327327 | AX327327 | Sequence |
| | 14 | 1212 | 52.2 | 1572 | 6 | AX359923 | AX359923 | Sequence |
| | 15 | 1147.8 | 49.5 | 2426 | 6 | AR541778 | AR541778 | Sequence |
| c | 16 | 957.6 | 41.3 | 88948 | 2 | AC008947 | AC008947 | Homo sapi |
| | 17 | 957.6 | 41.3 | 179513 | 9 | AC016612 | AC016612 | Homo sapi |
| | 18 | 944.8 | 40.7 | 1569 | 6 | AX155213 | AX155213 | Sequence |
| | 19 | 912.4 | 39.3 | 2210 | 10 | AK128903 | AK128903 | Mus muscu |
| | 20 | 912.2 | 39.3 | 2192 | 10 | BC034837 | BC034837 | Mus muscu |
| | 21 | 912.2 | 39.3 | 2196 | 10 | BC022134 | BC022134 | Mus muscu |
| | 22 | 910.8 | 39.3 | 2212 | 6 | AX155214 | AX155214 | Sequence |
| | 23 | 909.2 | 39.2 | 2228 | 10 | BC025940 | BC025940 | Mus muscu |
| | 24 | 905.8 | 39.0 | 1836 | 6 | CQ726650 | CQ726650 | Sequence |
| | 25 | 789 | 34.0 | 1569 | 6 | AX155216 | AX155216 | Sequence |
| | 26 | 595.4 | 25.7 | 148069 | 2 | AC025476 | AC025476 | Homo sapi |
| | 27 | 595.2 | 25.7 | 770 | 6 | AX136483 | AX136483 | Sequence |
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| | 29 | 593.4 | 25.6 | 1842 | 6 | AX747286 | AX747286 | Sequence |
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| | 31 | 592.2 | 25.5 | 102255 | 2 | AC026735 | AC026735 | Homo sapi |
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| | 33 | 575.4 | 24.8 | 5002 | 9 | AK125803 | AK125803 | Homo sapi |
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| | 35 | 573.4 | 24.7 | 3108 | 9 | BC035012 | BC035012 | Homo sapi |
| c | 36 | 538.8 | 23.2 | 148069 | 2 | AC025476 | AC025476 | Homo sapi |
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| c | 38 | 538.4 | 23.2 | 594 | 6 | BD123872 | BD123872 | Secretary |
| | 39 | 471.2 | 20.3 | 1885 | 5 | BC076709 | BC076709 | Xenopus t |
| | 40 | 468.6 | 20.2 | 1835 | 5 | CR760227 | CR760227 | Xenopus t |
| | 41 | 444.8 | 19.2 | 88948 | 2 | AC008947 | AC008947 | Homo sapi |
| | 42 | 434.2 | 18.7 | 1839 | 5 | BC082844 | BC082844 | Xenopus l |
| | 43 | 433.6 | 18.7 | 105885 | 9 | AC008860 | AC008860 | Homo sapi |
| c | 44 | 320.6 | 13.8 | 156499 | 2 | AC132893 | AC132893 | Mus muscu |
| | 45 | 308.2 | 13.3 | 251769 | 2 | AC117913 | AC117913 | Rattus no |
| | 46 | 308 | 13.3 | 156499 | 2 | AC132893 | AC132893 | Mus muscu |
| c | 47 | 245.2 | 10.6 | 211178 | 10 | AC139209 | AC139209 | Mus muscu |
| c | 48 | 239.2 | 10.3 | 125145 | 2 | AC022136 | AC022136 | Homo sapi |
| c | 49 | 239.2 | 10.3 | 165304 | 9 | AC112204 | AC112204 | Homo sapi |
| c | 50 | 238.8 | 10.3 | 507 | 6 | CQ337751 | CQ337751 | Sequence |
| c | 51 | 220 | 9.5 | 277 | 6 | CQ350335 | CQ350335 | Sequence |
| | 52 | 174 | 7.5 | 1879 | 5 | AF129809 | AF129809 | Gallus ga |
| | 53 | 167.2 | 7.2 | 3598 | 10 | AK128994 | AK128994 | Mus muscu |
| | 54 | 167.2 | 7.2 | 4185 | 10 | RNU07683 | U07683 | Rattus norv |
| | 55 | 165.6 | 7.1 | 2633 | 10 | RATCERUDPG | L21698 | Rat ceramid |
| | 56 | 164 | 7.1 | 2308 | 6 | AX305987 | AX305987 | Sequence |
| | 57 | 164 | 7.1 | 2308 | 10 | MMGCGTEX | X92122 | M.musculus |
| | 58 | 164 | 7.1 | 3439 | 10 | BC016885 | BC016885 | Mus muscu |
| | 59 | 161.2 | 6.9 | 1593 | 4 | AY135176 | AY135176 | Canis fam |
| | 60 | 159.8 | 6.9 | 1609 | 4 | AF129810 | AF129810 | Bos tauru |

| | | | | | | | |
|---|-----|-------|-----|--------|----|-----------|--------------------|
| | 61 | 158 | 6.8 | 291 | 6 | CQ740738 | CQ740738 Sequence |
| | 62 | 156.8 | 6.8 | 464 | 11 | G60984 | G60984 SHGC-84035 |
| c | 63 | 156.8 | 6.8 | 69315 | 5 | AL935277 | AL935277 Zebrafish |
| | 64 | 156.4 | 6.7 | 1671 | 4 | RABUGT2BB | L01082 Oryctolagus |
| | 65 | 156.2 | 6.7 | 239559 | 2 | AC095531 | AC095531 Rattus no |
| | 66 | 152.6 | 6.6 | 1662 | 9 | AF294902 | AF294902 Macaca mu |
| | 67 | 152.6 | 6.6 | 1753 | 9 | AF016310 | AF016310 Macaca fa |
| | 68 | 152 | 6.6 | 1768 | 9 | AF112113 | AF112113 Macaca fa |
| | 69 | 151.8 | 6.5 | 1832 | 4 | RABUGT2BA | L01081 Oryctolagus |
| | 70 | 151 | 6.5 | 2560 | 10 | BC027200 | BC027200 Mus muscu |
| | 71 | 148.4 | 6.4 | 2897 | 4 | RABUGT2BC | L01083 Oryctolagus |
| | 72 | 148.2 | 6.4 | 2108 | 9 | AF112112 | AF112112 Macaca fa |
| | 73 | 148 | 6.4 | 1716 | 10 | RNUDPGT | Y00156 Rat mRNA fo |
| | 74 | 148 | 6.4 | 1819 | 10 | RATGRT | M31109 Rat UDP-glu |
| | 75 | 148 | 6.4 | 2547 | 10 | AF175221 | AF175221 Cavia por |
| c | 76 | 147.2 | 6.3 | 169025 | 2 | CR545478 | CR545478 Danio rer |
| c | 77 | 147.2 | 6.3 | 179798 | 5 | BX284110 | BX284110 Zebrafish |
| | 78 | 146.6 | 6.3 | 1825 | 10 | AB034987 | AB034987 Cavia por |
| | 79 | 145.2 | 6.3 | 1961 | 6 | AX401727 | AX401727 Sequence |
| | 80 | 145.2 | 6.3 | 1961 | 10 | RATUDPGTP | M13506 Rat liver U |
| | 81 | 144.8 | 6.2 | 2520 | 10 | AB034988 | AB034988 Cavia por |
| | 82 | 144.6 | 6.2 | 1662 | 9 | AF294901 | AF294901 Macaca mu |
| | 83 | 144.2 | 6.2 | 1584 | 6 | AX497165 | AX497165 Sequence |
| | 84 | 144.2 | 6.2 | 2786 | 9 | AK025587 | AK025587 Homo sapi |
| | 85 | 144.2 | 6.2 | 3006 | 6 | AX497163 | AX497163 Sequence |
| | 86 | 143.2 | 6.2 | 1636 | 6 | AX327326 | AX327326 Sequence |
| | 87 | 143.2 | 6.2 | 1647 | 9 | AY542891 | AY542891 Homo sapi |
| | 88 | 143.2 | 6.2 | 2759 | 6 | AX395164 | AX395164 Sequence |
| | 89 | 143.2 | 6.2 | 2966 | 6 | AR447660 | AR447660 Sequence |
| | 90 | 143.2 | 6.2 | 2974 | 6 | AX376454 | AX376454 Sequence |
| | 91 | 143.2 | 6.2 | 2974 | 9 | AY358727 | AY358727 Homo sapi |
| | 92 | 143 | 6.2 | 2648 | 9 | MFU91582 | U91582 Macaca fasc |
| | 93 | 142 | 6.1 | 1858 | 10 | RATUDPA | M33746 Rat UDP glu |
| | 94 | 141.8 | 6.1 | 336 | 6 | AX307956 | AX307956 Sequence |
| | 95 | 141.8 | 6.1 | 1915 | 9 | AF401657 | AF401657 Macaca fa |
| | 96 | 141.8 | 6.1 | 1947 | 10 | RNU27518 | U27518 Rattus norv |
| | 97 | 141 | 6.1 | 1648 | 10 | BC028262 | BC028262 Mus muscu |
| | 98 | 140.2 | 6.0 | 2595 | 10 | BC058786 | BC058786 Mus muscu |
| | 99 | 140 | 6.0 | 2634 | 6 | AX827435 | AX827435 Sequence |
| | 100 | 140 | 6.0 | 2634 | 10 | RATUDPGTR | J02589 Rattus norv |
| | 101 | 139.8 | 6.0 | 1584 | 10 | AF184901 | AF184901 Mus muscu |
| | 102 | 139.8 | 6.0 | 1639 | 6 | AX548042 | AX548042 Sequence |
| | 103 | 139.8 | 6.0 | 2585 | 10 | BC048926 | BC048926 Mus muscu |
| | 104 | 139.8 | 6.0 | 125523 | 5 | BX248385 | BX248385 Zebrafish |
| | 105 | 139.6 | 6.0 | 1896 | 10 | BC078782 | BC078782 Rattus no |
| | 106 | 139.4 | 6.0 | 1858 | 10 | MMUDPGT | X06358 Mouse mRNA |
| | 107 | 139.4 | 6.0 | 1895 | 10 | BC019487 | BC019487 Mus muscu |
| | 108 | 139.2 | 6.0 | 1855 | 6 | CQ812293 | CQ812293 Sequence |
| | 109 | 139.2 | 6.0 | 1855 | 6 | CQ870648 | CQ870648 Sequence |
| | 110 | 139.2 | 6.0 | 1855 | 6 | AX336329 | AX336329 Sequence |
| | 111 | 139.2 | 6.0 | 1855 | 6 | AX336696 | AX336696 Sequence |
| | 112 | 139.2 | 6.0 | 1855 | 6 | AX409473 | AX409473 Sequence |
| | 113 | 139.2 | 6.0 | 1855 | 9 | HUMUDPGTA | J05428 Human 3,4-c |
| | 114 | 137.8 | 5.9 | 1831 | 10 | RRUGTGENE | X57565 Rattus norv |
| | 115 | 137.8 | 5.9 | 1891 | 10 | BC057169 | BC057169 Mus muscu |
| | 116 | 137.8 | 5.9 | 1895 | 10 | BC069923 | BC069923 Mus muscu |
| | 117 | 137.8 | 5.9 | 1903 | 10 | BC015272 | BC015272 Mus muscu |

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|-----|-------|-----|------|----|-----------|--------------------|
| 118 | 137 | 5.9 | 2125 | 5 | BC078212 | BC078212 Danio rer |
| 119 | 136.8 | 5.9 | 1846 | 10 | RNUDPGTR | X03478 Rat liver m |
| 120 | 136.4 | 5.9 | 1692 | 9 | BC075069 | BC075069 Homo sapi |
| 121 | 136.4 | 5.9 | 1844 | 10 | RNU06273 | U06273 Rattus norv |
| 122 | 136.4 | 5.9 | 2107 | 6 | AR168316 | AR168316 Sequence |
| 123 | 136.4 | 5.9 | 2107 | 9 | HSU59209 | U59209 Homo sapien |
| 124 | 136.4 | 5.9 | 2172 | 6 | CQ850790 | CQ850790 Sequence |
| 125 | 136.4 | 5.9 | 2172 | 9 | AK127970 | AK127970 Homo sapi |
| 126 | 136.4 | 5.9 | 2448 | 6 | AX335823 | AX335823 Sequence |
| 127 | 136.4 | 5.9 | 2448 | 6 | AX770547 | AX770547 Sequence |
| 128 | 136.4 | 5.9 | 2448 | 9 | HSU30930 | U30930 Human UDP-G |
| 129 | 136 | 5.9 | 1766 | 9 | BC030974 | BC030974 Homo sapi |
| 130 | 136 | 5.9 | 1854 | 6 | BD229166 | BD229166 Genotype |
| 131 | 136 | 5.9 | 1854 | 6 | AR349418 | AR349418 Sequence |
| 132 | 133.8 | 5.8 | 1650 | 6 | BD260955 | BD260955 Carbohydr |
| 133 | 133.8 | 5.8 | 1650 | 6 | AX040087 | AX040087 Sequence |
| 134 | 133.8 | 5.8 | 1894 | 9 | HSU62899 | U62899 Human ceram |
| 135 | 133.6 | 5.8 | 1976 | 5 | BX936208 | BX936208 Gallus ga |
| 136 | 133.4 | 5.8 | 1760 | 6 | CQ727328 | CQ727328 Sequence |
| 137 | 133.4 | 5.8 | 1766 | 9 | HSA6054 | AJ006054 Homo sapi |
| 138 | 132 | 5.7 | 1614 | 6 | AX958396 | AX958396 Sequence |
| 139 | 131.8 | 5.7 | 1851 | 9 | AF177272 | AF177272 Homo sapi |
| 140 | 131.8 | 5.7 | 2093 | 5 | BC076044 | BC076044 Danio rer |
| 141 | 131.6 | 5.7 | 1846 | 10 | RNU06274 | U06274 Rattus norv |
| 142 | 131.6 | 5.7 | 2079 | 9 | HSAJ5162 | AJ005162 Homo sapi |
| 143 | 131.6 | 5.7 | 2092 | 6 | BD229135 | BD229135 Genotype |
| 144 | 131.6 | 5.7 | 2092 | 6 | AR349387 | AR349387 Sequence |
| 145 | 131.6 | 5.7 | 2129 | 9 | BC026264 | BC026264 Homo sapi |
| 146 | 130.6 | 5.6 | 1649 | 9 | BC069441 | BC069441 Homo sapi |
| 147 | 130.6 | 5.6 | 2818 | 4 | OCU72742 | U72742 Oryctolagus |
| 148 | 130 | 5.6 | 2097 | 9 | AF064200 | AF064200 Homo sapi |
| 149 | 130 | 5.6 | 2123 | 6 | AX410640 | AX410640 Sequence |
| 150 | 130 | 5.6 | 2123 | 9 | HSU06641 | U06641 Human UDP g |
| 151 | 129 | 5.6 | 1722 | 9 | AF016492 | AF016492 Homo sapi |
| 152 | 129 | 5.6 | 2799 | 6 | AX411112 | AX411112 Sequence |
| 153 | 129 | 5.6 | 2799 | 9 | HSUGT2BIO | X63359 H.sapiens U |
| 154 | 128.6 | 5.5 | 1500 | 9 | AF177274 | AF177274 Homo sapi |
| 155 | 128.4 | 5.5 | 1976 | 6 | BD229238 | BD229238 Genotype |
| 156 | 128.4 | 5.5 | 1976 | 6 | AR349490 | AR349490 Sequence |
| 157 | 128.4 | 5.5 | 2075 | 9 | AF072223 | AF072223 Macaca fa |
| 158 | 128.4 | 5.5 | 2090 | 6 | AX410646 | AX410646 Sequence |
| 159 | 128.4 | 5.5 | 2090 | 9 | HSU08854 | U08854 Human UDP g |
| 160 | 128.4 | 5.5 | 2091 | 9 | AF081793 | AF081793 Homo sapi |
| 161 | 128.4 | 5.5 | 2092 | 9 | AF548389 | AF548389 Homo sapi |
| 162 | 128.4 | 5.5 | 2114 | 9 | AF180322 | AF180322 Homo sapi |
| 163 | 128.2 | 5.5 | 1822 | 5 | BC075289 | BC075289 Xenopus t |
| 164 | 128.2 | 5.5 | 3062 | 10 | BC028826 | BC028826 Mus muscu |
| 165 | 127.6 | 5.5 | 1413 | 6 | AR208679 | AR208679 Sequence |
| 166 | 127.6 | 5.5 | 1413 | 6 | AR490895 | AR490895 Sequence |
| 167 | 125.2 | 5.4 | 2093 | 6 | AX411198 | AX411198 Sequence |
| 168 | 125.2 | 5.4 | 2093 | 9 | HSUDPGT | Y00317 Human mRNA |
| 169 | 124.8 | 5.4 | 2816 | 4 | AF039138 | AF039138 Felis cat |
| 170 | 124.8 | 5.4 | 2821 | 4 | AF039137 | AF039137 Felis cat |
| 171 | 123.8 | 5.3 | 1895 | 5 | BC075892 | BC075892 Danio rer |
| 172 | 122.4 | 5.3 | 2103 | 10 | BC025795 | BC025795 Mus muscu |
| 173 | 121.6 | 5.2 | 1602 | 9 | AF360121 | AF360121 Macaca mu |
| 174 | 121.6 | 5.2 | 2349 | 4 | AB010872 | AB010872 Felis cat |

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|-------|-------|-----|--------|----|-----------|--------------------|
| 175 | 120.8 | 5.2 | 1590 | 4 | AF011902 | AF011902 Oryctolag |
| 176 | 120.6 | 5.2 | 1224 | 6 | AX958404 | AX958404 Sequence |
| 177 | 120 | 5.2 | 1647 | 9 | AF104339 | AF104339 Macaca fa |
| 178 | 119.6 | 5.2 | 1587 | 4 | CFA290948 | AJ290948 Canis fam |
| 179 | 119.6 | 5.2 | 2342 | 9 | AY435136 | AY435136 Homo sapi |
| 180 | 119.6 | 5.2 | 2351 | 6 | CQ720471 | CQ720471 Sequence |
| 181 | 119.6 | 5.2 | 2351 | 6 | AX706961 | AX706961 Sequence |
| 182 | 119.6 | 5.2 | 2351 | 6 | AX707891 | AX707891 Sequence |
| 183 | 119.6 | 5.2 | 2351 | 9 | HUMHUGBR1 | M57899 Human bilir |
| 184 | 119.2 | 5.1 | 1621 | 9 | AF104338 | AF104338 Macaca fa |
| 185 | 119 | 5.1 | 1961 | 5 | BC055635 | BC055635 Danio rer |
| 186 | 118.8 | 5.1 | 2396 | 9 | AF104336 | AF104336 Macaca fa |
| 187 | 117.6 | 5.1 | 2339 | 9 | AY435141 | AY435141 Homo sapi |
| 188 | 117.6 | 5.1 | 2440 | 9 | AF104337 | AF104337 Macaca fa |
| 189 | 116.8 | 5.0 | 1602 | 9 | AY029169 | AY029169 Macaca mu |
| 190 | 116.2 | 5.0 | 2196 | 10 | AY227201 | AY227201 Mus muscu |
| 191 | 116 | 5.0 | 2388 | 9 | BC019861 | BC019861 Homo sapi |
| 192 | 115.8 | 5.0 | 2422 | 6 | AX336711 | AX336711 Sequence |
| 193 | 115.8 | 5.0 | 2422 | 6 | AX409459 | AX409459 Sequence |
| 194 | 115.8 | 5.0 | 2422 | 9 | HUMUGT1FA | J04093 Homo sapien |
| 195 | 114.6 | 4.9 | 2216 | 10 | AY435129 | AY435129 Rattus no |
| 196 | 114.4 | 4.9 | 2345 | 9 | AY435138 | AY435138 Homo sapi |
| 197 | 114.4 | 4.9 | 2345 | 9 | AY435140 | AY435140 Homo sapi |
| 198 | 114.2 | 4.9 | 2333 | 9 | AY435142 | AY435142 Homo sapi |
| 199 | 113.2 | 4.9 | 2392 | 9 | S55985 | S55985 Homo sapien |
| 200 | 112.8 | 4.9 | 2345 | 9 | AY435139 | AY435139 Homo sapi |
| 201 | 112.8 | 4.9 | 2368 | 9 | HUMHUGBR2 | M57951 Human bilir |
| 202 | 112.6 | 4.9 | 1593 | 9 | HSU89508 | U89508 Human UDP-g |
| 203 | 112.6 | 4.9 | 2003 | 9 | AK025403 | AK025403 Homo sapi |
| 204 | 112.6 | 4.9 | 2333 | 9 | AY435137 | AY435137 Homo sapi |
| 205 | 112.6 | 4.9 | 2390 | 9 | BC069210 | BC069210 Homo sapi |
| 206 | 112.6 | 4.9 | 2423 | 9 | BC020971 | BC020971 Homo sapi |
| 207 | 111.8 | 4.8 | 1590 | 4 | AB008677 | AB008677 Bos tauru |
| 208 | 111.8 | 4.8 | 2219 | 10 | AY435131 | AY435131 Rattus no |
| 209 | 111.4 | 4.8 | 2320 | 6 | AX286762 | AX286762 Sequence |
| 210 | 111.4 | 4.8 | 2320 | 6 | AX286764 | AX286764 Sequence |
| 211 | 111.4 | 4.8 | 2320 | 6 | AX356964 | AX356964 Sequence |
| 212 | 111.4 | 4.8 | 2320 | 9 | AF056188 | AF056188 Homo sapi |
| 213 | 111.4 | 4.8 | 2333 | 9 | AY435144 | AY435144 Homo sapi |
| 214 | 111.4 | 4.8 | 2405 | 9 | BC058844 | BC058844 Homo sapi |
| 215 | 111.4 | 4.8 | 2585 | 6 | CQ796153 | CQ796153 Sequence |
| 216 | 111.4 | 4.8 | 2585 | 6 | CQ796154 | CQ796154 Sequence |
| 217 | 111.4 | 4.8 | 2585 | 6 | CQ796155 | CQ796155 Sequence |
| 218 | 111 | 4.8 | 1593 | 9 | AF030310 | AF030310 Homo sapi |
| 219 | 111 | 4.8 | 1593 | 9 | HSU89507 | U89507 Human UDP-g |
| 220 | 111 | 4.8 | 2333 | 9 | AY435143 | AY435143 Homo sapi |
| 221 | 111 | 4.8 | 2363 | 9 | AF462267 | AF462267 Homo sapi |
| 222 | 111 | 4.8 | 2394 | 9 | AF462268 | AF462268 Homo sapi |
| 223 | 109.8 | 4.7 | 2216 | 10 | AY435135 | AY435135 Rattus no |
| 224 | 109.8 | 4.7 | 2241 | 10 | AF461735 | AF461735 Rattus no |
| 225 | 109.6 | 4.7 | 1655 | 5 | PPL249081 | AJ249081 Pleuronec |
| 226 | 109.6 | 4.7 | 2287 | 4 | AB018477 | AB018477 Ovis arie |
| 227 | 109.6 | 4.7 | 211178 | 10 | AC139209 | AC139209 Mus muscu |
| 228 | 109.2 | 4.7 | 241472 | 5 | BX005027 | BX005027 Zebrafish |
| c 229 | 108.8 | 4.7 | 154733 | 2 | AC127462 | AC127462 Danio rer |
| c 230 | 108.8 | 4.7 | 247221 | 2 | BX470211 | BX470211 Danio rer |
| 231 | 108.4 | 4.7 | 2284 | 10 | AF461736 | AF461736 Rattus no |

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|-------|-------|-----|--------|----|-----------|--------------------|
| 232 | 108.2 | 4.7 | 2194 | 10 | MUSUGTBR | L02333 Murine bili |
| 233 | 108.2 | 4.7 | 2215 | 10 | S64760 | S64760 UGTBr1=UDP- |
| 234 | 108.2 | 4.7 | 2224 | 10 | AY227194 | AY227194 Mus muscu |
| 235 | 108 | 4.7 | 2190 | 10 | AY227200 | AY227200 Mus muscu |
| 236 | 108 | 4.7 | 2203 | 10 | BC019434 | BC019434 Mus muscu |
| 237 | 108 | 4.7 | 2215 | 10 | AK128918 | AK128918 Mus muscu |
| 238 | 106.8 | 4.6 | 2231 | 10 | AY435128 | AY435128 Rattus no |
| 239 | 106.8 | 4.6 | 2239 | 10 | RNU20551 | U20551 Rattus norv |
| 240 | 106.6 | 4.6 | 2219 | 10 | AY435134 | AY435134 Rattus no |
| 241 | 106.6 | 4.6 | 2225 | 10 | AY435130 | AY435130 Rattus no |
| 242 | 106.6 | 4.6 | 2282 | 10 | AF461738 | AF461738 Rattus no |
| 243 | 106.6 | 4.6 | 2285 | 10 | BC078732 | BC078732 Rattus no |
| 244 | 105.4 | 4.5 | 2194 | 10 | AB094481 | AB094481 Mus muscu |
| 245 | 105.4 | 4.5 | 2203 | 10 | AY227196 | AY227196 Mus muscu |
| 246 | 105.2 | 4.5 | 1968 | 5 | PPUGTMRN | X74116 P.platessa |
| 247 | 105 | 4.5 | 1765 | 10 | RATUDPGTA | M34007 Rat bilirub |
| 248 | 104.8 | 4.5 | 2155 | 10 | MUSUGTP | L27122 Mus musculu |
| 249 | 104.8 | 4.5 | 2236 | 5 | AB120133 | AB120133 Pleuronec |
| 250 | 104 | 4.5 | 151144 | 5 | BX323575 | BX323575 Zebrafish |
| 251 | 103.8 | 4.5 | 2219 | 10 | AY435132 | AY435132 Rattus no |
| 252 | 103.8 | 4.5 | 2297 | 10 | AF461734 | AF461734 Rattus no |
| 253 | 103.4 | 4.5 | 2037 | 4 | OCU09101 | U09101 Oryctolagus |
| 254 | 103.2 | 4.4 | 2193 | 10 | AY227199 | AY227199 Mus muscu |
| 255 | 101.6 | 4.4 | 1584 | 6 | CQ586740 | CQ586740 Sequence |
| 256 | 101.6 | 4.4 | 1602 | 10 | D87866 | D87866 Mus musculu |
| 257 | 101.6 | 4.4 | 1619 | 3 | AY070934 | AY070934 Drosophil |
| 258 | 101.6 | 4.4 | 2211 | 10 | AY227195 | AY227195 Mus muscu |
| c 259 | 101.6 | 4.4 | 3650 | 6 | CQ586739 | CQ586739 Sequence |
| c 260 | 101.6 | 4.4 | 164386 | 3 | AC006491 | AC006491 Drosophil |
| c 261 | 101.6 | 4.4 | 210298 | 3 | AE003690 | AE003690 Drosophil |
| 262 | 100.8 | 4.3 | 2332 | 4 | AB018478 | AB018478 Ovis arie |
| 263 | 100 | 4.3 | 1634 | 10 | MMU09930 | U09930 Mus musculu |
| c 264 | 100 | 4.3 | 24145 | 2 | AC014455 | AC014455 Drosophil |
| 265 | 98.8 | 4.3 | 1212 | 6 | CQ597654 | CQ597654 Sequence |
| 266 | 98.8 | 4.3 | 1704 | 6 | CQ600372 | CQ600372 Sequence |
| 267 | 98.8 | 4.3 | 1980 | 3 | BT006007 | BT006007 Drosophil |
| 268 | 98.8 | 4.3 | 1987 | 3 | AY060891 | AY060891 Drosophil |
| c 269 | 98.8 | 4.3 | 3212 | 6 | CQ597653 | CQ597653 Sequence |
| 270 | 98.8 | 4.3 | 4357 | 6 | CQ600371 | CQ600371 Sequence |
| 271 | 98.8 | 4.3 | 24145 | 2 | AC014455 | AC014455 Drosophil |
| 272 | 98.8 | 4.3 | 164386 | 3 | AC006491 | AC006491 Drosophil |
| 273 | 98.8 | 4.3 | 210298 | 3 | AE003690 | AE003690 Drosophil |
| 274 | 98.4 | 4.2 | 2290 | 10 | BC026561 | BC026561 Mus muscu |
| 275 | 98.4 | 4.2 | 2303 | 10 | BC069940 | BC069940 Mus muscu |
| 276 | 97.6 | 4.2 | 1458 | 6 | CQ590931 | CQ590931 Sequence |
| 277 | 97.6 | 4.2 | 3458 | 6 | CQ590930 | CQ590930 Sequence |
| 278 | 97.6 | 4.2 | 37688 | 2 | AL513222 | AL513222 Drosophil |
| 279 | 97.6 | 4.2 | 37688 | 3 | DMCEG0003 | AL031863 Drosophil |
| 280 | 97.6 | 4.2 | 95850 | 2 | AC020063 | AC020063 Drosophil |
| 281 | 97.6 | 4.2 | 154985 | 3 | AC004641 | AC004641 Drosophil |
| c 282 | 97.6 | 4.2 | 160338 | 3 | AC099021 | AC099021 Drosophil |
| c 283 | 97.6 | 4.2 | 272948 | 3 | AE003805 | AE003805 Drosophil |
| 284 | 97 | 4.2 | 1593 | 10 | D83796 | D83796 Rat UGT1 mR |
| 285 | 97 | 4.2 | 2216 | 10 | AY435133 | AY435133 Rattus no |
| 286 | 97 | 4.2 | 2343 | 10 | AF461737 | AF461737 Rattus no |
| 287 | 96.8 | 4.2 | 1596 | 10 | D87867 | D87867 Mus musculu |
| 288 | 96.8 | 4.2 | 2265 | 10 | AY227197 | AY227197 Mus muscu |

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|-------|------|-----|--------|----|----------|--------------------|
| 289 | 96.8 | 4.2 | 2300 | 10 | MMU16818 | U16818 Mus musculu |
| 290 | 96.8 | 4.2 | 120848 | 2 | AC007801 | AC007801 Drosophil |
| 291 | 95.6 | 4.1 | 735 | 6 | AR252918 | AR252918 Sequence |
| 292 | 95.4 | 4.1 | 1927 | 10 | RATUDPGT | J02612 Rat UDP-glu |
| 293 | 95.2 | 4.1 | 2248 | 10 | AY227198 | AY227198 Mus muscu |
| c 294 | 94.6 | 4.1 | 168062 | 2 | AC012857 | AC012857 Drosophil |
| 295 | 94.6 | 4.1 | 172479 | 3 | AC006590 | AC006590 Drosophil |
| 296 | 94.6 | 4.1 | 260027 | 3 | AE003659 | AE003659 Drosophil |
| 297 | 94 | 4.1 | 2055 | 4 | OCU09030 | U09030 Oryctolagus |
| 298 | 93.4 | 4.0 | 1560 | 6 | CQ586749 | CQ586749 Sequence |
| c 299 | 93.4 | 4.0 | 3828 | 6 | CQ586748 | CQ586748 Sequence |
| 300 | 93 | 4.0 | 1652 | 6 | CQ580647 | CQ580647 Sequence |
| 301 | 93 | 4.0 | 1766 | 3 | AY070917 | AY070917 Drosophil |
| c 302 | 93 | 4.0 | 3991 | 6 | CQ580646 | CQ580646 Sequence |
| c 303 | 93 | 4.0 | 14112 | 6 | CQ592361 | CQ592361 Sequence |
| c 304 | 93 | 4.0 | 19914 | 2 | AC018009 | AC018009 Drosophil |
| 305 | 93 | 4.0 | 177339 | 3 | AC008231 | AC008231 Drosophil |
| c 306 | 93 | 4.0 | 305150 | 3 | AE003453 | AE003453 Drosophil |
| 307 | 92.8 | 4.0 | 662 | 6 | AX525627 | AX525627 Sequence |
| 308 | 91.8 | 4.0 | 642 | 6 | AX526169 | AX526169 Sequence |
| 309 | 91.6 | 3.9 | 662 | 6 | AX525915 | AX525915 Sequence |
| 310 | 91.2 | 3.9 | 1662 | 9 | BC053576 | BC053576 Homo sapi |
| 311 | 91 | 3.9 | 1648 | 6 | CQ609717 | CQ609717 Sequence |
| 312 | 91 | 3.9 | 1692 | 3 | AY118747 | AY118747 Drosophil |
| 313 | 88.8 | 3.8 | 1673 | 3 | AY071256 | AY071256 Drosophil |
| c 314 | 88.8 | 3.8 | 5278 | 6 | CQ611354 | CQ611354 Sequence |
| c 315 | 88.8 | 3.8 | 77707 | 2 | AC014787 | AC014787 Drosophil |
| c 316 | 88.8 | 3.8 | 177480 | 3 | AC008287 | AC008287 Drosophil |
| c 317 | 88.8 | 3.8 | 225974 | 3 | AE003778 | AE003778 Drosophil |
| 318 | 88.2 | 3.8 | 2484 | 10 | RATUGT | J05132 Rat 3-methy |
| 319 | 87.4 | 3.8 | 1595 | 6 | CQ586224 | CQ586224 Sequence |
| 320 | 86.2 | 3.7 | 874 | 6 | AX421573 | AX421573 Sequence |
| 321 | 85.2 | 3.7 | 3716 | 6 | CQ614606 | CQ614606 Sequence |
| 322 | 82.6 | 3.6 | 1572 | 6 | CQ612552 | CQ612552 Sequence |
| 323 | 82.6 | 3.6 | 3572 | 6 | CQ612551 | CQ612551 Sequence |
| 324 | 82.6 | 3.6 | 60144 | 2 | AC019798 | AC019798 Drosophil |
| c 325 | 82.6 | 3.6 | 91685 | 2 | AC005121 | AC005121 Drosophil |
| 326 | 82.6 | 3.6 | 175413 | 3 | AC093097 | AC093097 Drosophil |
| 327 | 82.6 | 3.6 | 262525 | 3 | AE003652 | AE003652 Drosophil |
| c 328 | 80.8 | 3.5 | 4016 | 6 | CQ586223 | CQ586223 Sequence |
| c 329 | 80.8 | 3.5 | 163325 | 3 | AC008309 | AC008309 Drosophil |
| c 330 | 80.8 | 3.5 | 167475 | 3 | AC016132 | AC016132 Drosophil |
| 331 | 80.8 | 3.5 | 220936 | 2 | AC020256 | AC020256 Drosophil |
| c 332 | 80.8 | 3.5 | 241480 | 3 | AE003734 | AE003734 Drosophil |
| 333 | 80.6 | 3.5 | 1593 | 6 | CQ613314 | CQ613314 Sequence |
| 334 | 80.6 | 3.5 | 3659 | 6 | CQ613313 | CQ613313 Sequence |
| 335 | 80.6 | 3.5 | 174677 | 3 | AC018479 | AC018479 Drosophil |
| 336 | 80.6 | 3.5 | 193248 | 3 | AC007752 | AC007752 Drosophil |
| 337 | 80.6 | 3.5 | 221239 | 3 | AE003697 | AE003697 Drosophil |
| c 338 | 80.6 | 3.5 | 324288 | 2 | AC017336 | AC017336 Drosophil |
| 339 | 80 | 3.4 | 170142 | 9 | AP002383 | AP002383 Homo sapi |
| 340 | 80 | 3.4 | 174742 | 2 | AC016896 | AC016896 Homo sapi |
| 341 | 80 | 3.4 | 195466 | 2 | AC032024 | AC032024 Homo sapi |
| 342 | 79.4 | 3.4 | 1413 | 6 | CQ611790 | CQ611790 Sequence |
| 343 | 79.4 | 3.4 | 2820 | 6 | CQ611355 | CQ611355 Sequence |
| 344 | 79.2 | 3.4 | 7218 | 6 | I66494 | I66494 Sequence 14 |
| 345 | 78.8 | 3.4 | 804 | 6 | CQ727942 | CQ727942 Sequence |

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|-------|------|-----|--------|----|-----------|--------------------|
| 346 | 78.8 | 3.4 | 1988 | 3 | AY069392 | AY069392 Drosophil |
| 347 | 78.8 | 3.4 | 2437 | 3 | AY071467 | AY071467 Drosophil |
| 348 | 78.6 | 3.4 | 678 | 6 | AX526170 | AX526170 Sequence |
| c 349 | 78.6 | 3.4 | 235952 | 2 | AC110101 | AC110101 Rattus no |
| c 350 | 78.6 | 3.4 | 256974 | 2 | AC095475 | AC095475 Rattus no |
| c 351 | 78 | 3.4 | 195466 | 2 | AC032024 | AC032024 Homo sapi |
| 352 | 77.8 | 3.4 | 5205 | 6 | CQ609716 | CQ609716 Sequence |
| c 353 | 77.8 | 3.4 | 128469 | 2 | AC020029 | AC020029 Drosophil |
| 354 | 77.8 | 3.4 | 172061 | 3 | AC009203 | AC009203 Drosophil |
| 355 | 77.8 | 3.4 | 232737 | 3 | AE003660 | AE003660 Drosophil |
| 356 | 77.2 | 3.3 | 189 | 6 | CQ740741 | CQ740741 Sequence |
| 357 | 77 | 3.3 | 1352 | 10 | MMGCGTEX1 | X92123 M.musculus |
| 358 | 77 | 3.3 | 2023 | 10 | MMCGT2 | U48892 Mus musculu |
| 359 | 77 | 3.3 | 202752 | 2 | AC111106 | AC111106 Mus muscu |
| 360 | 76.6 | 3.3 | 696 | 6 | CQ734321 | CQ734321 Sequence |
| 361 | 76.4 | 3.3 | 169056 | 2 | CR381587 | CR381587 Danio rer |
| 362 | 74.6 | 3.2 | 603 | 6 | AX401758 | AX401758 Sequence |
| 363 | 74.6 | 3.2 | 603 | 10 | S56937 | S56937 3-methylcho |
| 364 | 74 | 3.2 | 582 | 6 | CQ458675 | CQ458675 Sequence |
| 365 | 73.8 | 3.2 | 4389 | 2 | AC014898 | AC014898 Drosophil |
| c 366 | 73.8 | 3.2 | 171334 | 3 | AC007477 | AC007477 Drosophil |
| c 367 | 73.8 | 3.2 | 196516 | 3 | AC013450 | AC013450 Drosophil |
| 368 | 73.8 | 3.2 | 280240 | 3 | AE003786 | AE003786 Drosophil |
| c 369 | 73.2 | 3.2 | 237028 | 2 | BX000470 | BX000470 Danio rer |
| 370 | 72.2 | 3.1 | 1443 | 9 | HSCGT01 | U31353 Human UDP-G |
| 371 | 72.2 | 3.1 | 149028 | 9 | AC122938 | AC122938 Homo sapi |
| 372 | 72 | 3.1 | 293 | 6 | CQ427045 | CQ427045 Sequence |
| 373 | 72 | 3.1 | 439 | 6 | CQ417459 | CQ417459 Sequence |
| 374 | 71.2 | 3.1 | 1681 | 3 | AF324465 | AF324465 Bombyx mo |
| 375 | 70.8 | 3.1 | 601 | 6 | AX401757 | AX401757 Sequence |
| 376 | 70.8 | 3.1 | 601 | 10 | S56936 | S56936 bilirubin-s |
| 377 | 70.2 | 3.0 | 246176 | 2 | AC114845 | AC114845 Rattus no |
| 378 | 69.4 | 3.0 | 1680 | 6 | CQ586665 | CQ586665 Sequence |
| 379 | 69.4 | 3.0 | 1781 | 3 | AY051661 | AY051661 Drosophil |
| 380 | 69.4 | 3.0 | 1782 | 6 | CQ586689 | CQ586689 Sequence |
| c 381 | 69.4 | 3.0 | 3741 | 6 | CQ586664 | CQ586664 Sequence |
| c 382 | 69.4 | 3.0 | 3849 | 6 | CQ586688 | CQ586688 Sequence |
| c 383 | 69.4 | 3.0 | 30221 | 2 | AC014454 | AC014454 Drosophil |
| c 384 | 69.4 | 3.0 | 165136 | 3 | AC007645 | AC007645 Drosophil |
| 385 | 69.2 | 3.0 | 1491 | 6 | CQ581757 | CQ581757 Sequence |
| 386 | 69.2 | 3.0 | 3784 | 6 | CQ581756 | CQ581756 Sequence |
| c 387 | 68.6 | 3.0 | 3595 | 6 | CQ613379 | CQ613379 Sequence |
| c 388 | 68.6 | 3.0 | 174677 | 3 | AC018479 | AC018479 Drosophil |
| c 389 | 68.6 | 3.0 | 193248 | 3 | AC007752 | AC007752 Drosophil |
| c 390 | 68.6 | 3.0 | 221239 | 3 | AE003697 | AE003697 Drosophil |
| c 391 | 68.6 | 3.0 | 246724 | 2 | AC131807 | AC131807 Rattus no |
| 392 | 68.6 | 3.0 | 324288 | 2 | AC017336 | AC017336 Drosophil |
| 393 | 68.2 | 2.9 | 769 | 6 | AR497103 | AR497103 Sequence |
| 394 | 68.2 | 2.9 | 769 | 6 | AR512385 | AR512385 Sequence |
| 395 | 68 | 2.9 | 1539 | 6 | CQ613380 | CQ613380 Sequence |
| 396 | 67.8 | 2.9 | 2972 | 14 | AF373031 | AF373031 Epinotia |
| c 397 | 67.4 | 2.9 | 224097 | 2 | AC117901 | AC117901 Rattus no |
| c 398 | 67.4 | 2.9 | 251769 | 2 | AC117913 | AC117913 Rattus no |
| 399 | 66.6 | 2.9 | 1793 | 3 | AF116555 | AF116555 Drosophil |
| 400 | 66.4 | 2.9 | 11728 | 10 | RATUDPGV | M74439 Rattus norv |
| c 401 | 66.4 | 2.9 | 138578 | 2 | AC141352 | AC141352 Rattus no |
| 402 | 66.4 | 2.9 | 146839 | 2 | AC142006 | AC142006 Rattus no |

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|-------|------|-----|--------|----|----------|----------|-------------|
| 403 | 66.2 | 2.9 | 1931 | 6 | CQ609720 | CQ609720 | Sequence |
| 404 | 66.2 | 2.9 | 1952 | 3 | AY051629 | AY051629 | Drosophil |
| 405 | 66 | 2.8 | 1188 | 6 | CQ597045 | CQ597045 | Sequence |
| c 406 | 66 | 2.8 | 3188 | 6 | CQ597044 | CQ597044 | Sequence |
| 407 | 66 | 2.8 | 42006 | 2 | AC018022 | AC018022 | Drosophil |
| c 408 | 66 | 2.8 | 162923 | 3 | AC008236 | AC008236 | Drosophil |
| c 409 | 66 | 2.8 | 210258 | 3 | AE003743 | AE003743 | Drosophil |
| 410 | 65.8 | 2.8 | 1672 | 6 | CQ598692 | CQ598692 | Sequence |
| 411 | 65.8 | 2.8 | 1946 | 3 | AY070939 | AY070939 | Drosophil |
| 412 | 65.8 | 2.8 | 3751 | 6 | CQ598691 | CQ598691 | Sequence |
| c 413 | 65.8 | 2.8 | 170362 | 3 | AC009250 | AC009250 | Drosophil |
| 414 | 65.6 | 2.8 | 179810 | 9 | AC139345 | AC139345 | Papio anu |
| 415 | 65.4 | 2.8 | 1488 | 6 | CQ597786 | CQ597786 | Sequence |
| 416 | 65.4 | 2.8 | 1584 | 6 | CQ609723 | CQ609723 | Sequence |
| 417 | 65.4 | 2.8 | 1920 | 3 | AY069532 | AY069532 | Drosophil |
| 418 | 65.4 | 2.8 | 1977 | 6 | CQ729719 | CQ729719 | Sequence |
| 419 | 65.4 | 2.8 | 3613 | 6 | CQ594473 | CQ594473 | Sequence |
| 420 | 65.4 | 2.8 | 4082 | 6 | CQ597785 | CQ597785 | Sequence |
| 421 | 65.4 | 2.8 | 4082 | 6 | CQ609722 | CQ609722 | Sequence |
| 422 | 65.4 | 2.8 | 167777 | 3 | AC009204 | AC009204 | Drosophil |
| 423 | 64.8 | 2.8 | 2216 | 10 | RATUDPB | M33747 | Rat UDP glu |
| 424 | 64.8 | 2.8 | 150430 | 10 | AC133491 | AC133491 | Rattus no |
| c 425 | 64.8 | 2.8 | 150430 | 10 | AC133491 | AC133491 | Rattus no |
| c 426 | 64.8 | 2.8 | 246176 | 2 | AC114845 | AC114845 | Rattus no |
| 427 | 64.8 | 2.8 | 246724 | 2 | AC131807 | AC131807 | Rattus no |
| c 428 | 64.6 | 2.8 | 1369 | 6 | AR508827 | AR508827 | Sequence |
| 429 | 64.6 | 2.8 | 1623 | 6 | CQ593769 | CQ593769 | Sequence |
| c 430 | 64.6 | 2.8 | 3683 | 6 | CQ593768 | CQ593768 | Sequence |
| 431 | 63.8 | 2.8 | 500 | 6 | CQ071564 | CQ071564 | Sequence |
| 432 | 63.8 | 2.8 | 500 | 6 | CQ102164 | CQ102164 | Sequence |
| 433 | 63.8 | 2.8 | 500 | 6 | CQ141114 | CQ141114 | Sequence |
| 434 | 63.8 | 2.8 | 500 | 6 | CQ176767 | CQ176767 | Sequence |
| 435 | 63.8 | 2.8 | 500 | 6 | CQ224383 | CQ224383 | Sequence |
| 436 | 63.8 | 2.8 | 500 | 6 | CQ262401 | CQ262401 | Sequence |
| 437 | 63.8 | 2.8 | 500 | 6 | CQ336589 | CQ336589 | Sequence |
| 438 | 63.8 | 2.8 | 689 | 6 | BD229133 | BD229133 | Genotype |
| 439 | 63.8 | 2.8 | 689 | 6 | AR349385 | AR349385 | Sequence |
| 440 | 63.8 | 2.8 | 1521 | 6 | CQ592386 | CQ592386 | Sequence |
| 441 | 63.8 | 2.8 | 3576 | 6 | CQ592385 | CQ592385 | Sequence |
| c 442 | 63.8 | 2.8 | 27310 | 9 | AF135416 | AF135416 | Homo sapi |
| c 443 | 63.8 | 2.8 | 103343 | 9 | AC108078 | AC108078 | Homo sapi |
| c 444 | 63.8 | 2.8 | 138232 | 2 | AC012582 | AC012582 | Homo sapi |
| c 445 | 63.8 | 2.8 | 226077 | 2 | AC013296 | AC013296 | Homo sapi |
| 446 | 63.6 | 2.7 | 145299 | 5 | BX005348 | BX005348 | Zebrafish |
| 447 | 63.6 | 2.7 | 229237 | 5 | BX323548 | BX323548 | Zebrafish |
| 448 | 63.6 | 2.7 | 238195 | 2 | CR790368 | CR790368 | Danio rer |
| 449 | 63.4 | 2.7 | 1367 | 9 | AY529122 | AY529122 | Homo sapi |
| 450 | 63.4 | 2.7 | 1755 | 3 | AY071432 | AY071432 | Drosophil |
| 451 | 63.4 | 2.7 | 21000 | 6 | AX395166 | AX395166 | Sequence |
| c 452 | 63.4 | 2.7 | 132963 | 2 | AC017518 | AC017518 | Drosophil |
| 453 | 63.4 | 2.7 | 146309 | 2 | CR388385 | CR388385 | Homo sapi |
| 454 | 63.4 | 2.7 | 173723 | 3 | AC009351 | AC009351 | Drosophil |
| 455 | 63.4 | 2.7 | 217991 | 9 | AC021146 | AC021146 | Homo sapi |
| 456 | 63.4 | 2.7 | 280096 | 3 | AE003613 | AE003613 | Drosophil |
| 457 | 63.2 | 2.7 | 1047 | 6 | CQ733586 | CQ733586 | Sequence |
| 458 | 62.6 | 2.7 | 521 | 10 | MMCGT5 | U48895 | Mus musculu |
| 459 | 62.6 | 2.7 | 156225 | 2 | AC115007 | AC115007 | Mus muscu |

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|-------|------|-----|--------|----|-----------|--------------------|
| 460 | 62.6 | 2.7 | 205079 | 10 | AC118544 | AC118544 Mus muscu |
| 461 | 62.6 | 2.7 | 240490 | 2 | AC100269 | AC100269 Mus muscu |
| 462 | 62.4 | 2.7 | 391 | 6 | BD237020 | BD237020 Compounds |
| 463 | 62.4 | 2.7 | 391 | 6 | AR225420 | AR225420 Sequence |
| 464 | 62.4 | 2.7 | 391 | 6 | AR562843 | AR562843 Sequence |
| 465 | 62.4 | 2.7 | 391 | 6 | AX321490 | AX321490 Sequence |
| 466 | 62.2 | 2.7 | 1443 | 6 | CQ595215 | CQ595215 Sequence |
| 467 | 62.2 | 2.7 | 1591 | 6 | BD229170 | BD229170 Genotype |
| 468 | 62.2 | 2.7 | 1591 | 6 | AR349422 | AR349422 Sequence |
| c 469 | 62.2 | 2.7 | 3495 | 6 | CQ595214 | CQ595214 Sequence |
| c 470 | 62.2 | 2.7 | 34551 | 2 | AC017171 | AC017171 Drosophil |
| c 471 | 62.2 | 2.7 | 78938 | 3 | AC002503 | AC002503 Drosophil |
| 472 | 62.2 | 2.7 | 104079 | 9 | AC107401 | AC107401 Homo sapi |
| 473 | 62.2 | 2.7 | 156578 | 9 | AC111000 | AC111000 Homo sapi |
| c 474 | 62.2 | 2.7 | 174735 | 3 | AC006402 | AC006402 Drosophil |
| c 475 | 62.2 | 2.7 | 182901 | 3 | AC093198 | AC093198 Drosophil |
| c 476 | 62.2 | 2.7 | 318278 | 3 | AE003666 | AE003666 Drosophil |
| 477 | 62 | 2.7 | 1543 | 9 | AF177273 | AF177273 Homo sapi |
| 478 | 62 | 2.7 | 2301 | 10 | RNU75903 | U75903 Rattus norv |
| 479 | 62 | 2.7 | 209071 | 3 | AC005285 | AC005285 Drosophil |
| 480 | 61.8 | 2.7 | 1527 | 6 | CQ580845 | CQ580845 Sequence |
| 481 | 61.8 | 2.7 | 1757 | 3 | AY128460 | AY128460 Drosophil |
| c 482 | 61.8 | 2.7 | 4647 | 6 | CQ580844 | CQ580844 Sequence |
| c 483 | 61.8 | 2.7 | 78277 | 2 | AC020206 | AC020206 Drosophil |
| 484 | 61.8 | 2.7 | 81677 | 3 | AC004377 | AC004377 Drosophil |
| c 485 | 61.8 | 2.7 | 169534 | 3 | AC008350 | AC008350 Drosophil |
| c 486 | 61.8 | 2.7 | 302225 | 3 | AE003458 | AE003458 Drosophil |
| 487 | 61.6 | 2.7 | 29546 | 3 | AY246561 | AY246561 Branchios |
| c 488 | 61.4 | 2.6 | 3679 | 6 | CQ593771 | CQ593771 Sequence |
| 489 | 61 | 2.6 | 851 | 11 | BV017252 | BV017252 S212P6006 |
| 490 | 60.8 | 2.6 | 1692 | 8 | AK109806 | AK109806 Oryza sat |
| c 491 | 60.8 | 2.6 | 141545 | 8 | OSJN00221 | AL663019 Oryza sat |
| c 492 | 60.6 | 2.6 | 43323 | 9 | AC114797 | AC114797 Homo sapi |
| 493 | 60.4 | 2.6 | 1500 | 6 | CQ614607 | CQ614607 Sequence |
| 494 | 60 | 2.6 | 220 | 6 | CQ080780 | CQ080780 Sequence |
| 495 | 60 | 2.6 | 220 | 6 | CQ115243 | CQ115243 Sequence |
| 496 | 60 | 2.6 | 220 | 6 | CQ154074 | CQ154074 Sequence |
| 497 | 60 | 2.6 | 220 | 6 | CQ186655 | CQ186655 Sequence |
| 498 | 60 | 2.6 | 220 | 6 | CQ237309 | CQ237309 Sequence |
| 499 | 60 | 2.6 | 220 | 6 | CQ274933 | CQ274933 Sequence |
| 500 | 60 | 2.6 | 220 | 6 | CQ349280 | CQ349280 Sequence |
| 501 | 60 | 2.6 | 402 | 10 | MMGCGTEX4 | X92126 M.musculus |
| 502 | 59.6 | 2.6 | 1668 | 6 | CQ586722 | CQ586722 Sequence |
| 503 | 59.6 | 2.6 | 1676 | 3 | AY051442 | AY051442 Drosophil |
| c 504 | 59.6 | 2.6 | 3740 | 6 | CQ586721 | CQ586721 Sequence |
| c 505 | 59.6 | 2.6 | 110907 | 14 | AY229987 | AY229987 Cryptophl |
| 506 | 59.4 | 2.6 | 1606 | 6 | AX675577 | AX675577 Sequence |
| 507 | 59.4 | 2.6 | 1606 | 6 | AX921811 | AX921811 Sequence |
| 508 | 59.4 | 2.6 | 176321 | 2 | BX942829 | BX942829 Danio rer |
| 509 | 59.4 | 2.6 | 186564 | 10 | AC119816 | AC119816 Mus muscu |
| 510 | 59.2 | 2.6 | 427 | 9 | HSCGT04 | U31861 Human UDP-g |
| c 511 | 59 | 2.5 | 589 | 6 | CQ225338 | CQ225338 Sequence |
| c 512 | 59 | 2.5 | 589 | 6 | CQ263337 | CQ263337 Sequence |
| 513 | 59 | 2.5 | 103343 | 9 | AC108078 | AC108078 Homo sapi |
| c 514 | 59 | 2.5 | 217991 | 9 | AC021146 | AC021146 Homo sapi |
| 515 | 58.6 | 2.5 | 1648 | 8 | AK064151 | AK064151 Oryza sat |
| 516 | 58.6 | 2.5 | 141040 | 8 | AP004382 | AP004382 Oryza sat |

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|-------|------|-----|--------|----|-----------|---------------------|
| 517 | 58 | 2.5 | 609 | 10 | RATUD2A07 | M35083 Rat UDP glu |
| 518 | 58 | 2.5 | 1704 | 3 | AF116554 | AF116554 Drosophil |
| 519 | 58 | 2.5 | 247575 | 2 | AC125632 | AC125632 Rattus no |
| 520 | 57.8 | 2.5 | 2108 | 14 | LOGVEGT | Y08294 Lacanobia o |
| c 521 | 57.8 | 2.5 | 145253 | 10 | AC138173 | AC138173 Mus muscu |
| c 522 | 57.8 | 2.5 | 186564 | 10 | AC119816 | AC119816 Mus muscu |
| c 523 | 57.4 | 2.5 | 831 | 6 | AR524865 | AR524865 Sequence |
| 524 | 57.4 | 2.5 | 2036 | 6 | CQ581913 | CQ581913 Sequence |
| 525 | 57.4 | 2.5 | 4386 | 6 | CQ581912 | CQ581912 Sequence |
| c 526 | 57.4 | 2.5 | 63705 | 9 | AF135419 | AF135419 sHomo sapi |
| 527 | 57.4 | 2.5 | 67568 | 2 | AC020378 | AC020378 Drosophil |
| c 528 | 57.4 | 2.5 | 123406 | 8 | AC120508 | AC120508 Oryza sat |
| 529 | 57.4 | 2.5 | 148977 | 9 | AC114786 | AC114786 Homo sapi |
| 530 | 57.2 | 2.5 | 149712 | 2 | AC140853 | AC140853 Canis fam |
| c 531 | 57.2 | 2.5 | 149712 | 2 | AC140853 | AC140853 Canis fam |
| 532 | 57.2 | 2.5 | 161844 | 2 | AC147451 | AC147451 Otolemur |
| c 533 | 57.2 | 2.5 | 208667 | 10 | AC101835 | AC101835 Mus muscu |
| 534 | 57 | 2.5 | 1665 | 8 | AB009370 | AB009370 Vigna mun |
| 535 | 56.8 | 2.4 | 1416 | 8 | MZEIAGLU | L34847 Zea mays IA |
| 536 | 56.8 | 2.4 | 1731 | 6 | AR260578 | AR260578 Sequence |
| 537 | 56.8 | 2.4 | 161046 | 14 | AF081810 | AF081810 Lymantria |
| 538 | 56.8 | 2.4 | 183755 | 2 | AC146742 | AC146742 Papio anu |
| c 539 | 56.8 | 2.4 | 183807 | 9 | AC091778 | AC091778 Papio anu |
| c 540 | 56.6 | 2.4 | 52742 | 2 | AC147071 | AC147071 Homo sapi |
| c 541 | 56.6 | 2.4 | 96776 | 9 | AC134921 | AC134921 Homo sapi |
| 542 | 56.6 | 2.4 | 165501 | 2 | AC147569 | AC147569 Homo sapi |
| c 543 | 56.6 | 2.4 | 184963 | 9 | AC147055 | AC147055 Homo sapi |
| 544 | 56.6 | 2.4 | 232016 | 2 | AC148029 | AC148029 Homo sapi |
| 545 | 56.2 | 2.4 | 513 | 6 | AR509041 | AR509041 Sequence |
| 546 | 56.2 | 2.4 | 983 | 6 | AR284336 | AR284336 Sequence |
| 547 | 56.2 | 2.4 | 4966 | 6 | CQ609719 | CQ609719 Sequence |
| c 548 | 56.2 | 2.4 | 160256 | 2 | CR753888 | CR753888 Danio rer |
| 549 | 56.2 | 2.4 | 183498 | 5 | BX072578 | BX072578 Zebrafish |
| c 550 | 56 | 2.4 | 183498 | 5 | BX072578 | BX072578 Zebrafish |
| 551 | 55.8 | 2.4 | 350 | 6 | AX887421 | AX887421 Sequence |
| 552 | 55.8 | 2.4 | 350 | 6 | BD027031 | BD027031 Sequence |
| c 553 | 55.6 | 2.4 | 106525 | 9 | AC093720 | AC093720 Homo sapi |
| 554 | 55.6 | 2.4 | 147009 | 2 | AC108490 | AC108490 Homo sapi |
| 555 | 55.6 | 2.4 | 153296 | 9 | AC147070 | AC147070 Homo sapi |
| 556 | 55.6 | 2.4 | 155175 | 2 | AC147064 | AC147064 Homo sapi |
| 557 | 55.6 | 2.4 | 181117 | 9 | AC019173 | AC019173 Homo sapi |
| c 558 | 55.4 | 2.4 | 590 | 11 | BV100588 | BV100588 RPAMSEQ0 |
| c 559 | 55.2 | 2.4 | 203 | 6 | CQ238174 | CQ238174 Sequence |
| c 560 | 55.2 | 2.4 | 203 | 6 | CQ275780 | CQ275780 Sequence |
| 561 | 55 | 2.4 | 1602 | 6 | BD229242 | BD229242 Genotype |
| 562 | 55 | 2.4 | 1602 | 6 | AR349494 | AR349494 Sequence |
| 563 | 55 | 2.4 | 106525 | 9 | AC093720 | AC093720 Homo sapi |
| 564 | 54.6 | 2.4 | 848 | 6 | CQ722622 | CQ722622 Sequence |
| 565 | 54.4 | 2.3 | 5122 | 14 | AY250076 | AY250076 Spodopter |
| 566 | 54.4 | 2.3 | 6120 | 8 | AF331855 | AF331855 Zea mays |
| 567 | 54.2 | 2.3 | 1933 | 9 | AK130038 | AK130038 Homo sapi |
| c 568 | 54.2 | 2.3 | 3642 | 6 | CQ611789 | CQ611789 Sequence |
| 569 | 54 | 2.3 | 245842 | 2 | AC106307 | AC106307 Rattus no |
| 570 | 53.8 | 2.3 | 138232 | 2 | AC012582 | AC012582 Homo sapi |
| c 571 | 53.8 | 2.3 | 169483 | 9 | AC093829 | AC093829 Homo sapi |
| 572 | 53.8 | 2.3 | 228873 | 2 | AC134364 | AC134364 Rattus no |
| c 573 | 53.8 | 2.3 | 231284 | 2 | AC095374 | AC095374 Rattus no |

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|-------|------|-----|--------|----|----------|--------------------|
| 574 | 53.6 | 2.3 | 1536 | 8 | AB027454 | AB027454 Petunia x |
| c 575 | 53.4 | 2.3 | 583 | 11 | BV100584 | BV100584 RPAMMSEQ0 |
| c 576 | 53.4 | 2.3 | 583 | 11 | BV163609 | BV163609 RPAMMSEQ0 |
| 577 | 53.4 | 2.3 | 784 | 6 | AX356966 | AX356966 Sequence |
| 578 | 53.4 | 2.3 | 784 | 9 | HUMUGT02 | M84123 Human UDP-g |
| 579 | 53.4 | 2.3 | 1620 | 6 | CQ593772 | CQ593772 Sequence |
| 580 | 53.4 | 2.3 | 16944 | 9 | AY603772 | AY603772 Homo sapi |
| c 581 | 53.4 | 2.3 | 23787 | 8 | AP005917 | AP005917 Oryza sat |
| c 582 | 53.4 | 2.3 | 68770 | 9 | AC006985 | AC006985 Homo sapi |
| c 583 | 53.4 | 2.3 | 176619 | 2 | AC026497 | AC026497 Homo sapi |
| 584 | 53.4 | 2.3 | 198872 | 9 | AF297093 | AF297093 Homo sapi |
| 585 | 53.2 | 2.3 | 1730 | 8 | AB070746 | AB070746 Vigna ang |
| 586 | 53 | 2.3 | 1813 | 8 | AY257207 | AY257207 Ipomoea t |
| 587 | 52.8 | 2.3 | 125020 | 9 | AF429315 | AF429315 Homo sapi |
| c 588 | 52.6 | 2.3 | 82746 | 1 | AF453501 | AF453501 Actinosyn |
| 589 | 52.4 | 2.3 | 209586 | 2 | AC148497 | AC148497 Otolemur |
| 590 | 52 | 2.2 | 707 | 6 | CQ492835 | CQ492835 Sequence |
| 591 | 52 | 2.2 | 90972 | 8 | AP006584 | AP006584 Oryza sat |
| c 592 | 52 | 2.2 | 122193 | 2 | AP006053 | AP006053 Oryza sat |
| 593 | 51.8 | 2.2 | 1584 | 8 | AB103471 | AB103471 Aralia co |
| c 594 | 51.6 | 2.2 | 576 | 11 | BV163611 | BV163611 RPAMMSEQ0 |
| 595 | 51.6 | 2.2 | 1594 | 8 | AB191247 | AB191247 Dianthus |
| 596 | 51.6 | 2.2 | 105931 | 2 | AC005427 | AC005427 Drosophil |
| c 597 | 51.6 | 2.2 | 176321 | 2 | BX942829 | BX942829 Danio rer |
| 598 | 51.4 | 2.2 | 1490 | 8 | AY257208 | AY257208 Ipomoea n |
| 599 | 51.4 | 2.2 | 1786 | 8 | AB038248 | AB038248 Ipomoea b |
| c 600 | 51.4 | 2.2 | 94516 | 8 | AP004526 | AP004526 Lotus cor |
| 601 | 51 | 2.2 | 1378 | 8 | AB070743 | AB070743 Vigna ang |
| c 602 | 51 | 2.2 | 1640 | 8 | AK099344 | AK099344 Oryza sat |
| 603 | 51 | 2.2 | 1686 | 8 | AK106005 | AK106005 Oryza sat |
| 604 | 51 | 2.2 | 1709 | 8 | AK105785 | AK105785 Oryza sat |
| c 605 | 51 | 2.2 | 1747 | 8 | AK064324 | AK064324 Oryza sat |
| c 606 | 51 | 2.2 | 1790 | 8 | AK101518 | AK101518 Oryza sat |
| 607 | 51 | 2.2 | 1862 | 8 | AK100744 | AK100744 Oryza sat |
| 608 | 51 | 2.2 | 124591 | 8 | AC118347 | AC118347 Oryza sat |
| c 609 | 51 | 2.2 | 146154 | 2 | AP004400 | AP004400 Oryza sat |
| c 610 | 51 | 2.2 | 156069 | 8 | AC136842 | AC136842 Oryza sat |
| 611 | 51 | 2.2 | 183095 | 8 | AP005186 | AP005186 Oryza sat |
| 612 | 50.8 | 2.2 | 1545 | 8 | AB191245 | AB191245 Dianthus |
| c 613 | 50.8 | 2.2 | 8596 | 14 | AF527603 | AF527603 Spodopter |
| c 614 | 50.8 | 2.2 | 38383 | 3 | CEF35H8 | Z36752 Caenorhabdi |
| c 615 | 50.8 | 2.2 | 146839 | 2 | AC142006 | AC142006 Rattus no |
| c 616 | 50.6 | 2.2 | 1105 | 8 | AK060146 | AK060146 Oryza sat |
| c 617 | 50.6 | 2.2 | 124366 | 8 | AC131374 | AC131374 Oryza sat |
| c 618 | 50.6 | 2.2 | 300029 | 8 | AE017077 | AE017077 Oryza sat |
| 619 | 50.4 | 2.2 | 1391 | 6 | CQ774188 | CQ774188 Sequence |
| 620 | 50.4 | 2.2 | 1494 | 6 | AX652909 | AX652909 Sequence |
| 621 | 50.4 | 2.2 | 1733 | 8 | AK106250 | AK106250 Oryza sat |
| 622 | 50.4 | 2.2 | 1795 | 8 | AK066593 | AK066593 Oryza sat |
| 623 | 50.4 | 2.2 | 1999 | 6 | AX756082 | AX756082 Sequence |
| 624 | 50.4 | 2.2 | 1999 | 8 | AK066469 | AK066469 Oryza sat |
| 625 | 50.4 | 2.2 | 131616 | 6 | CQ774045 | CQ774045 Sequence |
| c 626 | 50.4 | 2.2 | 131680 | 14 | AY522332 | AY522332 Agrotis s |
| c 627 | 50.4 | 2.2 | 147472 | 8 | AP003974 | AP003974 Oryza sat |
| c 628 | 50.4 | 2.2 | 147739 | 8 | AP005915 | AP005915 Oryza sat |
| 629 | 50.2 | 2.2 | 1577 | 8 | AK107669 | AK107669 Oryza sat |
| 630 | 50.2 | 2.2 | 1662 | 8 | AB070754 | AB070754 Vigna ang |

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|-------|------|-----|--------|----|-----------|----------|-------------|
| 631 | 50.2 | 2.2 | 1843 | 8 | AK065112 | AK065112 | Oryza sat |
| 632 | 50.2 | 2.2 | 58309 | 8 | AP006173 | AP006173 | Oryza sat |
| c 633 | 50.2 | 2.2 | 185449 | 8 | AC123526 | AC123526 | Oryza sat |
| 634 | 49.8 | 2.1 | 1086 | 8 | AY257215 | AY257215 | Ipomoea a |
| 635 | 49.8 | 2.1 | 6322 | 8 | AF331854 | AF331854 | Zea mays |
| c 636 | 49.8 | 2.1 | 140023 | 4 | AC093453 | AC093453 | Canis fam |
| 637 | 49.6 | 2.1 | 563 | 6 | CQ505416 | CQ505416 | Sequence |
| 638 | 49.4 | 2.1 | 1578 | 6 | E12713 | E12713 | Solanum mel |
| 639 | 49.4 | 2.1 | 1578 | 8 | SMGT | X77369 | S.melongena |
| c 640 | 49.4 | 2.1 | 2850 | 14 | SLPVEGT | X99073 | Spodoptera |
| 641 | 49.2 | 2.1 | 656 | 6 | AX201693 | AX201693 | Sequence |
| 642 | 49.2 | 2.1 | 657 | 6 | AR307005 | AR307005 | Sequence |
| 643 | 49.2 | 2.1 | 657 | 6 | AX154755 | AX154755 | Sequence |
| 644 | 49.2 | 2.1 | 1109 | 3 | AY069046 | AY069046 | Drosophil |
| 645 | 49.2 | 2.1 | 1530 | 6 | CQ612555 | CQ612555 | Sequence |
| 646 | 49.2 | 2.1 | 1752 | 6 | CQ600621 | CQ600621 | Sequence |
| 647 | 49.2 | 2.1 | 3679 | 6 | CQ612554 | CQ612554 | Sequence |
| c 648 | 49.2 | 2.1 | 5189 | 14 | SLAJ3131 | AJ003131 | Spodopter |
| 649 | 49 | 2.1 | 501 | 6 | CQ475453 | CQ475453 | Sequence |
| 650 | 49 | 2.1 | 18314 | 3 | AF125959 | AF125959 | Caenorhab |
| 651 | 49 | 2.1 | 158826 | 8 | AP003607 | AP003607 | Oryza sat |
| c 652 | 49 | 2.1 | 175667 | 8 | AC119147 | AC119147 | Genomic s |
| c 653 | 49 | 2.1 | 189057 | 2 | BX957337 | BX957337 | Danio rer |
| 654 | 48.8 | 2.1 | 1141 | 6 | AX083744 | AX083744 | Sequence |
| 655 | 48.8 | 2.1 | 1496 | 8 | AY262037 | AY262037 | Crocus sa |
| 656 | 48.8 | 2.1 | 1689 | 14 | LDU04321 | U04321 | Lymantria d |
| c 657 | 48.6 | 2.1 | 666 | 6 | AX660993 | AX660993 | Sequence |
| 658 | 48.6 | 2.1 | 1001 | 6 | AR284354 | AR284354 | Sequence |
| 659 | 48.6 | 2.1 | 1501 | 8 | AK059016 | AK059016 | Oryza sat |
| 660 | 48.6 | 2.1 | 1684 | 8 | AB070755 | AB070755 | Vigna ang |
| c 661 | 48.6 | 2.1 | 2000 | 6 | AX655393 | AX655393 | Sequence |
| 662 | 48.6 | 2.1 | 2031 | 8 | AK067710 | AK067710 | Oryza sat |
| 663 | 48.4 | 2.1 | 789 | 6 | AX660822 | AX660822 | Sequence |
| 664 | 48.4 | 2.1 | 1437 | 6 | AX505505 | AX505505 | Sequence |
| 665 | 48.4 | 2.1 | 1455 | 6 | AX654659 | AX654659 | Sequence |
| 666 | 48.4 | 2.1 | 1464 | 8 | BT015770 | BT015770 | Arabidops |
| 667 | 48.4 | 2.1 | 1724 | 8 | AY049277 | AY049277 | Arabidops |
| 668 | 48.4 | 2.1 | 1727 | 8 | AK071819 | AK071819 | Oryza sat |
| 669 | 48.4 | 2.1 | 1781 | 14 | MBU41999 | U41999 | Mamestra br |
| 670 | 48.4 | 2.1 | 2396 | 6 | E25788 | E25788 | Ecdysteroid |
| c 671 | 48.4 | 2.1 | 84196 | 8 | ATT3A5 | AL132979 | Arabidops |
| c 672 | 48.4 | 2.1 | 89469 | 8 | ATF18B3 | AL049862 | Arabidops |
| c 673 | 48.4 | 2.1 | 110086 | 8 | AP003373 | AP003373 | Oryza sat |
| 674 | 48.4 | 2.1 | 153656 | 14 | AF539999 | AF539999 | Mamestra |
| 675 | 48.4 | 2.1 | 155060 | 14 | MBU59461 | U59461 | Mamestra co |
| 676 | 48.2 | 2.1 | 1159 | 8 | AY257209 | AY257209 | Ipomoea.p |
| 677 | 48.2 | 2.1 | 1346 | 8 | AY257206 | AY257206 | Ipomoea h |
| c 678 | 48.2 | 2.1 | 206924 | 10 | AC087780 | AC087780 | Mus muscu |
| 679 | 48 | 2.1 | 1689 | 8 | AY087431 | AY087431 | Arabidops |
| 680 | 48 | 2.1 | 4354 | 5 | PPL249082 | AJ249082 | Pleuronec |
| c 681 | 48 | 2.1 | 130037 | 8 | AP004192 | AP004192 | Oryza sat |
| c 682 | 48 | 2.1 | 139342 | 14 | AF325155 | AF325155 | Spodopter |
| c 683 | 48 | 2.1 | 160215 | 10 | AC092531 | AC092531 | Rattus no |
| 684 | 48 | 2.1 | 164263 | 8 | AP005515 | AP005515 | Oryza sat |
| 685 | 48 | 2.1 | 185139 | 8 | AP004348 | AP004348 | Oryza sat |
| c 686 | 48 | 2.1 | 251485 | 2 | AC107287 | AC107287 | Rattus no |
| c 687 | 48 | 2.1 | 256354 | 10 | AC120922 | AC120922 | Rattus no |

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|-------|------|-----|--------|----|-------------|--------------------|
| 688 | 47.8 | 2.1 | 1138 | 6 | AX432482 | AX432482 Sequence |
| 689 | 47.8 | 2.1 | 1785 | 8 | AK105261 | AK105261 Oryza sat |
| 690 | 47.8 | 2.1 | 1896 | 8 | AK101659 | AK101659 Oryza sat |
| 691 | 47.8 | 2.1 | 1896 | 8 | AK103824 | AK103824 Oryza sat |
| 692 | 47.8 | 2.1 | 110000 | 1 | AE017333_08 | Continuation (9 of |
| 693 | 47.8 | 2.1 | 110000 | 1 | CP000002_08 | Continuation (9 of |
| 694 | 47.8 | 2.1 | 146154 | 2 | AP004400 | AP004400 Oryza sat |
| c 695 | 47.8 | 2.1 | 183095 | 8 | AP005186 | AP005186 Oryza sat |
| 696 | 47.6 | 2.1 | 1925 | 14 | SLNPVEGT | X84701 Spodoptera |
| 697 | 47.4 | 2.0 | 1410 | 6 | AX653349 | AX653349 Sequence |
| 698 | 47.4 | 2.0 | 1729 | 8 | AK060965 | AK060965 Oryza sat |
| 699 | 47.4 | 2.0 | 135323 | 8 | CNS08CBQ | AL928753 Oryza sat |
| 700 | 47.2 | 2.0 | 1609 | 8 | AB070757 | AB070757 Vigna ang |
| c 701 | 47 | 2.0 | 137678 | 8 | AP005183 | AP005183 Oryza sat |
| c 702 | 47 | 2.0 | 138653 | 8 | AP005178 | AP005178 Oryza sat |
| 703 | 46.8 | 2.0 | 998 | 8 | AJ619862 | AJ619862 Arabidops |
| 704 | 46.8 | 2.0 | 998 | 8 | AJ619867 | AJ619867 Arabidops |
| 705 | 46.8 | 2.0 | 998 | 8 | AJ619868 | AJ619868 Arabidops |
| 706 | 46.8 | 2.0 | 998 | 8 | AJ619875 | AJ619875 Arabidops |
| 707 | 46.8 | 2.0 | 998 | 8 | AJ619876 | AJ619876 Arabidops |
| 708 | 46.8 | 2.0 | 998 | 8 | AJ619877 | AJ619877 Arabidops |
| 709 | 46.8 | 2.0 | 998 | 8 | AJ619878 | AJ619878 Arabidops |
| 710 | 46.8 | 2.0 | 1000 | 8 | AJ619869 | AJ619869 Arabidops |
| 711 | 46.8 | 2.0 | 1000 | 8 | AJ619870 | AJ619870 Arabidops |
| 712 | 46.8 | 2.0 | 1000 | 8 | AJ619871 | AJ619871 Arabidops |
| 713 | 46.8 | 2.0 | 1000 | 8 | AJ619872 | AJ619872 Arabidops |
| 714 | 46.8 | 2.0 | 1000 | 8 | AJ619873 | AJ619873 Arabidops |
| 715 | 46.8 | 2.0 | 1000 | 8 | AJ619879 | AJ619879 Arabidops |
| 716 | 46.8 | 2.0 | 1000 | 8 | AJ619880 | AJ619880 Arabidops |
| 717 | 46.8 | 2.0 | 1002 | 8 | AJ619874 | AJ619874 Arabidops |
| 718 | 46.8 | 2.0 | 158482 | 14 | AY126275 | AY126275 Mamestra |
| 719 | 46.6 | 2.0 | 1494 | 8 | AF028237 | AF028237 Ipomoea p |
| 720 | 46.6 | 2.0 | 2531 | 8 | ZMMC2BZ1 | X13501 Maize (Bz-M |
| 721 | 46.6 | 2.0 | 2919 | 8 | ZMMCCBZ1 | X13500 Zea mays (B |
| 722 | 46.6 | 2.0 | 4294 | 8 | AY191009 | AY191009 Zea mays |
| 723 | 46.6 | 2.0 | 5772 | 8 | AF355378 | AF355378 Zea mays |
| 724 | 46.6 | 2.0 | 41355 | 3 | U42832 | U42832 Caenorhabdi |
| 725 | 46.6 | 2.0 | 106186 | 8 | AF448416 | AF448416 Zea mays |
| 726 | 46.6 | 2.0 | 146949 | 2 | AL360003 | AL360003 Homo sapi |
| 727 | 46.6 | 2.0 | 150771 | 9 | AL392106 | AL392106 Human DNA |
| 728 | 46.6 | 2.0 | 226001 | 8 | AF391808 | AF391808 Zea mays |
| c 729 | 46.6 | 2.0 | 236362 | 2 | AC006724 | AC006724 Caenorhab |
| 730 | 46.4 | 2.0 | 470 | 11 | BX322426 | BX322426 Arabidops |
| 731 | 46.4 | 2.0 | 1440 | 6 | AX211632 | AX211632 Sequence |
| c 732 | 46.4 | 2.0 | 1440 | 6 | AX211634 | AX211634 Sequence |
| 733 | 46.4 | 2.0 | 1440 | 6 | AX505385 | AX505385 Sequence |
| 734 | 46.4 | 2.0 | 1471 | 8 | AY142676 | AY142676 Arabidops |
| 735 | 46.4 | 2.0 | 1599 | 8 | AK065987 | AK065987 Oryza sat |
| 736 | 46.4 | 2.0 | 1615 | 8 | AY074339 | AY074339 Arabidops |
| 737 | 46.4 | 2.0 | 1621 | 8 | AY057646 | AY057646 Arabidops |
| 738 | 46.4 | 2.0 | 1645 | 8 | AK105912 | AK105912 Oryza sat |
| 739 | 46.4 | 2.0 | 1645 | 8 | AK119544 | AK119544 Oryza sat |
| c 740 | 46.4 | 2.0 | 1657 | 8 | AY099833 | AY099833 Arabidops |
| 741 | 46.4 | 2.0 | 1683 | 8 | AK106006 | AK106006 Oryza sat |
| 742 | 46.4 | 2.0 | 138141 | 8 | AP005190 | AP005190 Oryza sat |
| c 743 | 46.4 | 2.0 | 168354 | 8 | AP005185 | AP005185 Oryza sat |
| c 744 | 46.4 | 2.0 | 197419 | 8 | ATCHRIV41 | AL161541 Arabidops |

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|-------|------|-----|--------|----|-----------|--------------------|
| c 745 | 46.4 | 2.0 | 205065 | 8 | ATFCA4 | Z97339 Arabidopsis |
| c 746 | 46.4 | 2.0 | 250029 | 3 | AE014820 | AE014820 Plasmodiu |
| c 747 | 46.4 | 2.0 | 287560 | 1 | AE017274 | AE017274 Bacillus |
| 748 | 46.2 | 2.0 | 467 | 11 | BV008367 | BV008367 MASC_STS1 |
| c 749 | 46.2 | 2.0 | 490 | 6 | CQ431226 | CQ431226 Sequence |
| 750 | 46.2 | 2.0 | 1458 | 6 | AX654445 | AX654445 Sequence |
| 751 | 46.2 | 2.0 | 1464 | 6 | AX653704 | AX653704 Sequence |
| c 752 | 46.2 | 2.0 | 1638 | 8 | AK105478 | AK105478 Oryza sat |
| 753 | 46.2 | 2.0 | 1663 | 8 | AK062590 | AK062590 Oryza sat |
| 754 | 46.2 | 2.0 | 1914 | 8 | AK068586 | AK068586 Oryza sat |
| c 755 | 46.2 | 2.0 | 134534 | 2 | AP004327 | AP004327 Oryza sat |
| c 756 | 46.2 | 2.0 | 140769 | 8 | AP003508 | AP003508 Oryza sat |
| c 757 | 46.2 | 2.0 | 141036 | 2 | AP003941 | AP003941 Oryza sat |
| c 758 | 46.2 | 2.0 | 150455 | 8 | AP004571 | AP004571 Oryza sat |
| c 759 | 46.2 | 2.0 | 162520 | 8 | AP005913 | AP005913 Oryza sat |
| c 760 | 46.2 | 2.0 | 165630 | 8 | AP003617 | AP003617 Oryza sat |
| c 761 | 46.2 | 2.0 | 166005 | 8 | AC120506 | AC120506 Oryza sat |
| c 762 | 46.2 | 2.0 | 194284 | 5 | AL954329 | AL954329 Zebrafish |
| 763 | 46 | 2.0 | 1259 | 8 | MECGT6 | X77463 M.esculenta |
| 764 | 46 | 2.0 | 1477 | 6 | CQ595878 | CQ595878 Sequence |
| 765 | 46 | 2.0 | 1553 | 8 | AK060228 | AK060228 Oryza sat |
| 766 | 46 | 2.0 | 1680 | 8 | AK069049 | AK069049 Oryza sat |
| c 767 | 46 | 2.0 | 1852 | 8 | AK105674 | AK105674 Oryza sat |
| 768 | 46 | 2.0 | 3528 | 6 | CQ595877 | CQ595877 Sequence |
| c 769 | 46 | 2.0 | 20493 | 2 | AC014076 | AC014076 Drosophil |
| c 770 | 46 | 2.0 | 138141 | 8 | AP005190 | AP005190 Oryza sat |
| 771 | 46 | 2.0 | 148780 | 3 | AC008326 | AC008326 Drosophil |
| c 772 | 46 | 2.0 | 156983 | 8 | OSJN00212 | AL663014 Oryza sat |
| c 773 | 46 | 2.0 | 164263 | 8 | AP005515 | AP005515 Oryza sat |
| c 774 | 46 | 2.0 | 168759 | 8 | AC079887 | AC079887 Oryza sat |
| 775 | 46 | 2.0 | 267997 | 3 | AE003616 | AE003616 Drosophil |
| 776 | 45.8 | 2.0 | 1395 | 6 | AX654788 | AX654788 Sequence |
| 777 | 45.8 | 2.0 | 1783 | 8 | AK108674 | AK108674 Oryza sat |
| 778 | 45.8 | 2.0 | 5908 | 1 | AF147704 | AF147704 Streptomy |
| 779 | 45.8 | 2.0 | 13511 | 6 | AX345183 | AX345183 Sequence |
| 780 | 45.8 | 2.0 | 18585 | 6 | AX281498 | AX281498 Sequence |
| c 781 | 45.8 | 2.0 | 138155 | 2 | AC151564 | AC151564 Dasypus n |
| c 782 | 45.8 | 2.0 | 191765 | 8 | AC129717 | AC129717 Oryza sat |
| 783 | 45.6 | 2.0 | 1510 | 8 | AK121682 | AK121682 Oryza sat |
| 784 | 45.6 | 2.0 | 1639 | 8 | AK105398 | AK105398 Oryza sat |
| c 785 | 45.6 | 2.0 | 1689 | 8 | AK063307 | AK063307 Oryza sat |
| 786 | 45.6 | 2.0 | 1750 | 8 | AK119905 | AK119905 Oryza sat |
| 787 | 45.6 | 2.0 | 32784 | 3 | CEF08G5 | Z70682 Caenorhabdi |
| c 788 | 45.6 | 2.0 | 97352 | 8 | AC091670 | AC091670 Oryza sat |
| 789 | 45.6 | 2.0 | 133889 | 8 | AC133334 | AC133334 Oryza sat |
| 790 | 45.4 | 2.0 | 1688 | 8 | AK107291 | AK107291 Oryza sat |
| 791 | 45.4 | 2.0 | 1706 | 8 | AK072018 | AK072018 Oryza sat |
| 792 | 45.4 | 2.0 | 105227 | 8 | AP005296 | AP005296 Oryza sat |
| 793 | 45.4 | 2.0 | 119926 | 8 | AP003705 | AP003705 Oryza sat |
| 794 | 45.4 | 2.0 | 135611 | 14 | AF169823 | AF169823 Spodopter |
| 795 | 45.4 | 2.0 | 137967 | 2 | AC093094 | AC093094 Oryza sat |
| c 796 | 45.4 | 2.0 | 165307 | 2 | AC123749 | AC123749 Mus muscu |
| 797 | 45.2 | 1.9 | 994 | 8 | AJ619855 | AJ619855 Arabidops |
| 798 | 45.2 | 1.9 | 994 | 8 | AJ619856 | AJ619856 Arabidops |
| 799 | 45.2 | 1.9 | 1383 | 6 | AX653292 | AX653292 Sequence |
| 800 | 45.2 | 1.9 | 1452 | 6 | AX653929 | AX653929 Sequence |
| c 801 | 45.2 | 1.9 | 1463 | 8 | AK108695 | AK108695 Oryza sat |

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|-------|------|-----|--------|----|------------|--------------------|
| 802 | 45.2 | 1.9 | 1549 | 6 | AX660242 | AX660242 Sequence |
| 803 | 45.2 | 1.9 | 1603 | 8 | AK107156 | AK107156 Oryza sat |
| 804 | 45.2 | 1.9 | 1736 | 8 | BT009372 | BT009372 Triticum |
| 805 | 45.2 | 1.9 | 1809 | 8 | AK103303 | AK103303 Oryza sat |
| 806 | 45.2 | 1.9 | 2000 | 6 | AX656006 | AX656006 Sequence |
| c 807 | 45.2 | 1.9 | 157987 | 8 | AP003560 | AP003560 Oryza sat |
| 808 | 45.2 | 1.9 | 163095 | 8 | AP002523 | AP002523 Oryza sat |
| 809 | 45 | 1.9 | 45 | 6 | AX697217 | AX697217 Sequence |
| 810 | 45 | 1.9 | 955 | 8 | AB012115 | AB012115 Vigna mun |
| 811 | 45 | 1.9 | 1521 | 8 | AY167672 | AY167672 Zea mays |
| 812 | 45 | 1.9 | 1521 | 8 | AY167673 | AY167673 Zea mays |
| 813 | 45 | 1.9 | 1521 | 8 | AY167675 | AY167675 Zea mays |
| 814 | 45 | 1.9 | 1521 | 8 | AY167676 | AY167676 Zea mays |
| 815 | 45 | 1.9 | 1521 | 8 | AY167679 | AY167679 Zea mays |
| 816 | 45 | 1.9 | 1536 | 6 | E49073 | E49073 UDP-D-Gluco |
| 817 | 45 | 1.9 | 1561 | 8 | AB191249 | AB191249 Dianthus |
| 818 | 45 | 1.9 | 1575 | 8 | AB002818 | AB002818 Perilla f |
| 819 | 45 | 1.9 | 1594 | 8 | ZMW22BZ1 | X13502 Maize (Bz-W |
| 820 | 45 | 1.9 | 1732 | 6 | E49068 | E49068 UDP-D-Gluco |
| 821 | 45 | 1.9 | 1732 | 8 | AB033758 | AB033758 Citrus un |
| 822 | 45 | 1.9 | 2908 | 8 | ZMBZW22 | X07937 Maize Bz-W2 |
| 823 | 45 | 1.9 | 3181 | 8 | ZMBZR | X07941 Maize bronz |
| c 824 | 45 | 1.9 | 37329 | 3 | U97009 | U97009 Caenorhabdi |
| 825 | 45 | 1.9 | 103960 | 8 | ATAC011664 | AC011664 Arabidops |
| 826 | 45 | 1.9 | 147472 | 8 | AP003974 | AP003974 Oryza sat |
| c 827 | 45 | 1.9 | 149227 | 2 | AC146976 | AC146976 Zea mays |
| c 828 | 45 | 1.9 | 179810 | 9 | AC139345 | AC139345 Papio anu |
| c 829 | 45 | 1.9 | 288479 | 2 | AC146814 | AC146814 Zea mays |
| c 830 | 44.8 | 1.9 | 774 | 6 | BD019848 | BD019848 Novel gen |
| c 831 | 44.8 | 1.9 | 774 | 6 | BD099786 | BD099786 Novel gen |
| 832 | 44.8 | 1.9 | 858 | 10 | RATUGT1B3G | D38067 Rattus norv |
| 833 | 44.8 | 1.9 | 995 | 8 | AJ619882 | AJ619882 Arabidops |
| 834 | 44.8 | 1.9 | 995 | 8 | AJ619883 | AJ619883 Arabidops |
| 835 | 44.8 | 1.9 | 1362 | 6 | AX412617 | AX412617 Sequence |
| 836 | 44.8 | 1.9 | 1362 | 6 | AX507722 | AX507722 Sequence |
| 837 | 44.8 | 1.9 | 1362 | 6 | AX589823 | AX589823 Sequence |
| 838 | 44.8 | 1.9 | 1362 | 6 | AX652007 | AX652007 Sequence |
| 839 | 44.8 | 1.9 | 1521 | 8 | AK110892 | AK110892 Oryza sat |
| 840 | 44.8 | 1.9 | 1787 | 8 | AF303396 | AF303396 Phaseolus |
| c 841 | 44.8 | 1.9 | 78089 | 3 | AC024876 | AC024876 Caenorhab |
| c 842 | 44.8 | 1.9 | 95824 | 9 | AC068888 | AC068888 Homo sapi |
| c 843 | 44.8 | 1.9 | 103223 | 8 | AC007153 | AC007153 Arabidops |
| 844 | 44.8 | 1.9 | 110000 | 2 | AC109940_0 | AC109940 Rattus no |
| 845 | 44.8 | 1.9 | 192969 | 2 | AC150463 | AC150463 Callithri |
| 846 | 44.8 | 1.9 | 221618 | 10 | AC092530 | AC092530 Rattus no |
| c 847 | 44.8 | 1.9 | 224007 | 2 | AC111764 | AC111764 Rattus no |
| c 848 | 44.8 | 1.9 | 298804 | 2 | AC006911 | AC006911 Caenorhab |
| 849 | 44.8 | 1.9 | 299081 | 2 | AC006892 | AC006892 Caenorhab |
| 850 | 44.6 | 1.9 | 762 | 6 | BD224494 | BD224494 Materials |
| 851 | 44.6 | 1.9 | 762 | 6 | AR216544 | AR216544 Sequence |
| c 852 | 44.6 | 1.9 | 1141 | 6 | AX083744 | AX083744 Sequence |
| 853 | 44.6 | 1.9 | 1558 | 8 | AB070748 | AB070748 Vigna ang |
| 854 | 44.6 | 1.9 | 1662 | 8 | AK064105 | AK064105 Oryza sat |
| 855 | 44.6 | 1.9 | 2591 | 8 | AK106639 | AK106639 Oryza sat |
| 856 | 44.6 | 1.9 | 110000 | 1 | AE017263_2 | Continuation (3 of |
| c 857 | 44.6 | 1.9 | 159861 | 8 | AP005012 | AP005012 Oryza sat |
| 858 | 44.6 | 1.9 | 287476 | 1 | AE017271 | AE017271 Bacillus |

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|-------|------|-----|--------|----|------------|----------|-------------|
| 859 | 44.4 | 1.9 | 1175 | 8 | AB074489 | AB074489 | Malus x d |
| 860 | 44.4 | 1.9 | 54025 | 8 | AP006525 | AP006525 | Oryza sat |
| 861 | 44.2 | 1.9 | 1666 | 8 | AK106038 | AK106038 | Oryza sat |
| c 862 | 44.2 | 1.9 | 133427 | 2 | AC134521 | AC134521 | Medicago |
| c 863 | 44.2 | 1.9 | 144271 | 8 | AC098682 | AC098682 | Genomic s |
| 864 | 44.2 | 1.9 | 302524 | 8 | AE017075 | AE017075 | Oryza sat |
| 865 | 44 | 1.9 | 1895 | 8 | AK108846 | AK108846 | Oryza sat |
| 866 | 44 | 1.9 | 3986 | 8 | AY490797 | AY490797 | Helianthu |
| 867 | 44 | 1.9 | 4556 | 9 | AF153832S3 | AF153834 | Homo sapi |
| c 868 | 44 | 1.9 | 144392 | 9 | HS67K17 | AL023584 | Human DNA |
| 869 | 44 | 1.9 | 148762 | 8 | AP002843 | AP002843 | Oryza sat |
| c 870 | 44 | 1.9 | 172752 | 2 | AC116496 | AC116496 | Mus muscu |
| 871 | 44 | 1.9 | 236164 | 2 | AC113057 | AC113057 | Mus muscu |
| 872 | 43.8 | 1.9 | 432 | 6 | A63526 | A63526 | Sequence 7 |
| 873 | 43.8 | 1.9 | 1152 | 6 | AX653506 | AX653506 | Sequence |
| 874 | 43.8 | 1.9 | 1482 | 6 | AX653177 | AX653177 | Sequence |
| 875 | 43.8 | 1.9 | 1654 | 8 | AK121725 | AK121725 | Oryza sat |
| 876 | 43.8 | 1.9 | 1660 | 8 | AB070745 | AB070745 | Vigna ang |
| 877 | 43.8 | 1.9 | 1726 | 8 | AK064395 | AK064395 | Oryza sat |
| 878 | 43.8 | 1.9 | 1798 | 8 | AY663785 | AY663785 | Fragaria |
| 879 | 43.8 | 1.9 | 1958 | 8 | AY171598 | AY171598 | Fragaria |
| 880 | 43.8 | 1.9 | 37845 | 3 | CEF01D4 | Z81054 | Caenorhabdi |
| c 881 | 43.8 | 1.9 | 46394 | 3 | CBRG17D06 | AC084511 | Caenorhab |
| 882 | 43.8 | 1.9 | 134534 | 2 | AP004327 | AP004327 | Oryza sat |
| 883 | 43.8 | 1.9 | 141036 | 2 | AP003941 | AP003941 | Oryza sat |
| 884 | 43.8 | 1.9 | 165630 | 8 | AP003617 | AP003617 | Oryza sat |
| c 885 | 43.8 | 1.9 | 182870 | 3 | AC116960 | AC116960 | Dictyoste |
| 886 | 43.8 | 1.9 | 184645 | 2 | AC108395 | AC108395 | Mus muscu |
| 887 | 43.8 | 1.9 | 349954 | 6 | AX196297 | AX196297 | Sequence |
| 888 | 43.6 | 1.9 | 617 | 12 | AY199453 | AY199453 | Arabidops |
| 889 | 43.6 | 1.9 | 993 | 8 | AJ619881 | AJ619881 | Arabidops |
| 890 | 43.6 | 1.9 | 993 | 8 | AJ619884 | AJ619884 | Arabidops |
| 891 | 43.6 | 1.9 | 993 | 8 | AJ619885 | AJ619885 | Arabidops |
| 892 | 43.6 | 1.9 | 994 | 8 | AJ619857 | AJ619857 | Arabidops |
| 893 | 43.6 | 1.9 | 994 | 8 | AJ619858 | AJ619858 | Arabidops |
| 894 | 43.6 | 1.9 | 994 | 8 | AJ619859 | AJ619859 | Arabidops |
| 895 | 43.6 | 1.9 | 994 | 8 | AJ619860 | AJ619860 | Arabidops |
| 896 | 43.6 | 1.9 | 994 | 8 | AJ619861 | AJ619861 | Arabidops |
| 897 | 43.6 | 1.9 | 994 | 8 | AJ619863 | AJ619863 | Arabidops |
| 898 | 43.6 | 1.9 | 994 | 8 | AJ619864 | AJ619864 | Arabidops |
| 899 | 43.6 | 1.9 | 994 | 8 | AJ619865 | AJ619865 | Arabidops |
| 900 | 43.6 | 1.9 | 994 | 8 | AJ619866 | AJ619866 | Arabidops |
| 901 | 43.6 | 1.9 | 1001 | 6 | AR284363 | AR284363 | Sequence |
| 902 | 43.6 | 1.9 | 1001 | 6 | AR284364 | AR284364 | Sequence |
| 903 | 43.6 | 1.9 | 1001 | 6 | AR284365 | AR284365 | Sequence |
| 904 | 43.6 | 1.9 | 1001 | 6 | AR284367 | AR284367 | Sequence |
| 905 | 43.6 | 1.9 | 1021 | 6 | BD229240 | BD229240 | Genotype |
| 906 | 43.6 | 1.9 | 1021 | 6 | AR349492 | AR349492 | Sequence |
| 907 | 43.6 | 1.9 | 1073 | 8 | MECGT2 | X77461 | M.esculenta |
| 908 | 43.6 | 1.9 | 1350 | 6 | AX412670 | AX412670 | Sequence |
| 909 | 43.6 | 1.9 | 1350 | 6 | AX507107 | AX507107 | Sequence |
| 910 | 43.6 | 1.9 | 1350 | 6 | AX651538 | AX651538 | Sequence |
| 911 | 43.6 | 1.9 | 1350 | 8 | BT010327 | BT010327 | Arabidops |
| 912 | 43.6 | 1.9 | 1437 | 6 | CQ759478 | CQ759478 | Sequence |
| 913 | 43.6 | 1.9 | 1437 | 6 | AX211615 | AX211615 | Sequence |
| 914 | 43.6 | 1.9 | 1527 | 8 | AY087340 | AY087340 | Arabidops |
| 915 | 43.6 | 1.9 | 1565 | 8 | AY087866 | AY087866 | Arabidops |

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|---|-----|------|-----|--------|----|-------------|--------------------|
| | 916 | 43.6 | 1.9 | 1582 | 8 | AY062483 | AY062483 Arabidops |
| c | 917 | 43.6 | 1.9 | 98734 | 8 | AC002333 | AC002333 Arabidops |
| | 918 | 43.6 | 1.9 | 103785 | 8 | ATF1I16 | AL161667 Arabidops |
| | 919 | 43.6 | 1.9 | 110036 | 8 | AC142095 | AC142095 Medicago |
| c | 920 | 43.6 | 1.9 | 203301 | 2 | AC147067 | AC147067 Homo sapi |
| | 921 | 43.4 | 1.9 | 929 | 8 | AK059765 | AK059765 Oryza sat |
| | 922 | 43.4 | 1.9 | 1359 | 6 | AX654630 | AX654630 Sequence |
| | 923 | 43.4 | 1.9 | 1521 | 8 | AY167674 | AY167674 Zea mays |
| | 924 | 43.4 | 1.9 | 1521 | 8 | AY167677 | AY167677 Zea mays |
| | 925 | 43.4 | 1.9 | 1521 | 8 | AY167678 | AY167678 Zea mays |
| | 926 | 43.4 | 1.9 | 1604 | 8 | AK106312 | AK106312 Oryza sat |
| | 927 | 43.4 | 1.9 | 1621 | 8 | AK100189 | AK100189 Oryza sat |
| | 928 | 43.4 | 1.9 | 4296 | 8 | AK068604 | AK068604 Oryza sat |
| | 929 | 43.4 | 1.9 | 8867 | 8 | AY191010 | AY191010 Zea mays |
| | 930 | 43.4 | 1.9 | 114283 | 2 | AC149822 | AC149822 Zea mays |
| | 931 | 43.4 | 1.9 | 148191 | 8 | OSJN00067 | AL606602 Oryza sat |
| | 932 | 43.4 | 1.9 | 149049 | 8 | AP004340 | AP004340 Oryza sat |
| c | 933 | 43.4 | 1.9 | 157452 | 2 | AC087800 | AC087800 Mus muscu |
| | 934 | 43.4 | 1.9 | 163032 | 8 | AP004263 | AP004263 Oryza sat |
| | 935 | 43.2 | 1.9 | 1001 | 6 | AR284366 | AR284366 Sequence |
| | 936 | 43.2 | 1.9 | 1546 | 8 | AK068362 | AK068362 Oryza sat |
| | 937 | 43.2 | 1.9 | 10329 | 6 | AX347024 | AX347024 Sequence |
| c | 938 | 43.2 | 1.9 | 43154 | 3 | U55369 | U55369 Caenorhabdi |
| c | 939 | 43.2 | 1.9 | 103234 | 2 | AP003997 | AP003997 Oryza sat |
| c | 940 | 43.2 | 1.9 | 128955 | 8 | AP003754 | AP003754 Oryza sat |
| c | 941 | 43.2 | 1.9 | 141040 | 8 | AP004382 | AP004382 Oryza sat |
| c | 942 | 43.2 | 1.9 | 146951 | 8 | AP003270 | AP003270 Oryza sat |
| c | 943 | 43.2 | 1.9 | 157248 | 8 | AP004300 | AP004300 Oryza sat |
| | 944 | 43.2 | 1.9 | 226077 | 2 | AC013296 | AC013296 Homo sapi |
| | 945 | 43.2 | 1.9 | 229569 | 2 | AC107424 | AC107424 Homo sapi |
| c | 946 | 43.2 | 1.9 | 251131 | 2 | AC111217 | AC111217 Rattus no |
| | 947 | 43.2 | 1.9 | 349980 | 6 | AX344569 | AX344569 Sequence |
| | 948 | 43.2 | 1.9 | 349980 | 6 | AX344570 | AX344570 Sequence |
| | 949 | 43.2 | 1.9 | 349980 | 6 | AX344573 | AX344573 Sequence |
| | 950 | 43.2 | 1.9 | 349980 | 6 | AX344574 | AX344574 Sequence |
| c | 951 | 43 | 1.9 | 340 | 8 | AY027263 | AY027263 Arabidops |
| | 952 | 43 | 1.9 | 393 | 6 | AX660985 | AX660985 Sequence |
| c | 953 | 43 | 1.9 | 469 | 11 | BV009002 | BV009002 MASC_STS1 |
| c | 954 | 43 | 1.9 | 519 | 11 | BV008995 | BV008995 MASC_STS1 |
| | 955 | 43 | 1.9 | 1350 | 6 | CQ759477 | CQ759477 Sequence |
| | 956 | 43 | 1.9 | 1440 | 8 | AF190634 | AF190634 Nicotiana |
| | 957 | 43 | 1.9 | 110000 | 1 | AE017180_09 | Continuation (10 o |
| | 958 | 43 | 1.9 | 142376 | 8 | AF503433 | AF503433 Sorghum b |
| | 959 | 42.8 | 1.8 | 1476 | 6 | AX653505 | AX653505 Sequence |
| | 960 | 42.8 | 1.8 | 1597 | 8 | AK068878 | AK068878 Oryza sat |
| | 961 | 42.8 | 1.8 | 1637 | 14 | AF313417 | AF313417 Anticarsi |
| | 962 | 42.8 | 1.8 | 1819 | 8 | AF117267 | AF117267 Malus dom |
| c | 963 | 42.8 | 1.8 | 35033 | 3 | AF067615 | AF067615 Caenorhab |
| c | 964 | 42.8 | 1.8 | 100999 | 14 | AF270937 | AF270937 Plutella |
| c | 965 | 42.8 | 1.8 | 124526 | 8 | AC146585 | AC146585 Medicago |
| | 966 | 42.8 | 1.8 | 131689 | 9 | AC010588 | AC010588 Homo sapi |
| | 967 | 42.8 | 1.8 | 161658 | 9 | AC008505 | AC008505 Homo sapi |
| c | 968 | 42.8 | 1.8 | 168753 | 9 | AC006120 | AC006120 Homo sapi |
| c | 969 | 42.8 | 1.8 | 276829 | 2 | AC006741 | AC006741 Caenorhab |
| | 970 | 42.6 | 1.8 | 432 | 5 | PFL291986 | AJ291986 Platichth |
| | 971 | 42.6 | 1.8 | 1368 | 6 | AX766275 | AX766275 Sequence |
| | 972 | 42.6 | 1.8 | 1760 | 8 | AK099049 | AK099049 Oryza sat |

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|-------|------|-----|--------|----|-----------|--------------------|
| 973 | 42.6 | 1.8 | 1761 | 8 | AK066462 | AK066462 Oryza sat |
| 974 | 42.6 | 1.8 | 2025 | 6 | AR152488 | AR152488 Sequence |
| 975 | 42.6 | 1.8 | 2025 | 6 | BD005789 | BD005789 Biologica |
| 976 | 42.6 | 1.8 | 2025 | 14 | HZU89958 | U89958 Helicoverpa |
| 977 | 42.6 | 1.8 | 2505 | 14 | AF503939 | AF503939 Helicover |
| 978 | 42.6 | 1.8 | 27908 | 3 | CET04H1 | Z78200 Caenorhabdi |
| 979 | 42.6 | 1.8 | 31495 | 14 | AF275264 | AF275264 Helicover |
| c 980 | 42.6 | 1.8 | 84203 | 8 | AC005106 | AC005106 Genomic s |
| c 981 | 42.6 | 1.8 | 87577 | 2 | BX640459 | BX640459 Danio rer |
| 982 | 42.6 | 1.8 | 114078 | 2 | BX640498 | BX640498 Danio rer |
| c 983 | 42.6 | 1.8 | 121889 | 5 | BX255952 | BX255952 Zebrafish |
| c 984 | 42.6 | 1.8 | 122128 | 8 | CNS07YPV | AL731761 Oryza sat |
| 985 | 42.6 | 1.8 | 130759 | 14 | AF303045 | AF303045 Helicover |
| 986 | 42.6 | 1.8 | 130869 | 14 | AF334030 | AF334030 Helicover |
| 987 | 42.6 | 1.8 | 131403 | 14 | AF271059 | AF271059 Helicove |
| c 988 | 42.6 | 1.8 | 158158 | 8 | AC146522 | AC146522 Oryza sat |
| 989 | 42.6 | 1.8 | 195190 | 2 | AC110843 | AC110843 Rattus no |
| c 990 | 42.6 | 1.8 | 246998 | 2 | CR450707 | CR450707 Danio rer |
| 991 | 42.6 | 1.8 | 250621 | 2 | CR792433 | CR792433 Danio rer |
| 992 | 42.4 | 1.8 | 121 | 6 | AX266625 | AX266625 Sequence |
| c 993 | 42.4 | 1.8 | 121 | 6 | AX266626 | AX266626 Sequence |
| 994 | 42.4 | 1.8 | 1410 | 6 | AX211623 | AX211623 Sequence |
| c 995 | 42.4 | 1.8 | 1410 | 6 | AX211625 | AX211625 Sequence |
| 996 | 42.4 | 1.8 | 1410 | 6 | AX720222 | AX720222 Sequence |
| 997 | 42.4 | 1.8 | 1410 | 6 | AX766274 | AX766274 Sequence |
| 998 | 42.4 | 1.8 | 1410 | 8 | AY078051 | AY078051 Arabidops |
| 999 | 42.4 | 1.8 | 1428 | 6 | AX507686 | AX507686 Sequence |
| 1000 | 42.4 | 1.8 | 1428 | 8 | BT012573 | BT012573 Arabidops |
| 1001 | 42.4 | 1.8 | 1430 | 6 | AX211635 | AX211635 Sequence |
| c1002 | 42.4 | 1.8 | 1430 | 6 | AX211637 | AX211637 Sequence |
| 1003 | 42.4 | 1.8 | 1437 | 8 | AY663786 | AY663786 Fragaria |
| 1004 | 42.4 | 1.8 | 1560 | 6 | AX412846 | AX412846 Sequence |
| 1005 | 42.4 | 1.8 | 1563 | 6 | AX654346 | AX654346 Sequence |
| 1006 | 42.4 | 1.8 | 1592 | 8 | AF196777 | AF196777 Arabidops |
| 1007 | 42.4 | 1.8 | 1597 | 8 | AF367358 | AF367358 Arabidops |
| 1008 | 42.4 | 1.8 | 1705 | 8 | AK099145 | AK099145 Oryza sat |
| 1009 | 42.4 | 1.8 | 1719 | 8 | AK070110 | AK070110 Oryza sat |
| 1010 | 42.4 | 1.8 | 1776 | 8 | AK059031 | AK059031 Oryza sat |
| 1011 | 42.4 | 1.8 | 2000 | 6 | AX655393 | AX655393 Sequence |
| 1012 | 42.4 | 1.8 | 91841 | 10 | AL606971 | AL606971 Mouse DNA |
| c1013 | 42.4 | 1.8 | 126497 | 9 | AC019044 | AC019044 Homo sapi |
| c1014 | 42.4 | 1.8 | 130779 | 8 | OSJN00283 | AL731638 Oryza sat |
| c1015 | 42.4 | 1.8 | 141883 | 8 | OSJN00271 | AL731626 Oryza sat |
| c1016 | 42.4 | 1.8 | 148191 | 8 | OSJN00067 | AL606602 Oryza sat |
| c1017 | 42.4 | 1.8 | 156649 | 8 | AC144738 | AC144738 Oryza sat |
| c1018 | 42.4 | 1.8 | 157648 | 2 | BX901886 | BX901886 Danio rer |
| c1019 | 42.4 | 1.8 | 164896 | 2 | CR762432 | CR762432 Danio rer |
| 1020 | 42.4 | 1.8 | 168759 | 8 | AC079887 | AC079887 Oryza sat |
| 1021 | 42.4 | 1.8 | 180557 | 9 | AC007250 | AC007250 Homo sapi |
| c1022 | 42.4 | 1.8 | 197061 | 10 | AL606914 | AL606914 Mouse DNA |
| 1023 | 42.4 | 1.8 | 301450 | 1 | AP003185 | AP003185 Clostridi |
| c1024 | 42.2 | 1.8 | 708 | 5 | AF352753 | AF352753 Oncorhync |
| 1025 | 42.2 | 1.8 | 1734 | 8 | AK060513 | AK060513 Oryza sat |
| 1026 | 42.2 | 1.8 | 2438 | 8 | AF426026 | AF426026 Piromyces |
| 1027 | 42.2 | 1.8 | 11319 | 1 | AE010792 | AE010792 Methanosa |
| 1028 | 42.2 | 1.8 | 40862 | 6 | AX346975 | AX346975 Sequence |
| 1029 | 42.2 | 1.8 | 70746 | 2 | AC150844 | AC150844 Medicago |

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|-------|------|-----|--------|----|------------|--------------------|
| c1030 | 42.2 | 1.8 | 75840 | 8 | AF527807 | AF527807 Sorghum b |
| 1031 | 42.2 | 1.8 | 117124 | 8 | AP006360 | AP006360 Lotus cor |
| c1032 | 42.2 | 1.8 | 165501 | 2 | AC147569 | AC147569 Homo sapi |
| 1033 | 42.2 | 1.8 | 191821 | 9 | AC022616 | AC022616 Homo sapi |
| 1034 | 42 | 1.8 | 408 | 6 | AR496501 | AR496501 Sequence |
| 1035 | 42 | 1.8 | 408 | 6 | AR511783 | AR511783 Sequence |
| 1036 | 42 | 1.8 | 1521 | 14 | AY048771 | AY048771 Bombyx mo |
| 1037 | 42 | 1.8 | 1800 | 6 | AR362648 | AR362648 Sequence |
| 1038 | 42 | 1.8 | 2793 | 6 | AR027919 | AR027919 Sequence |
| 1039 | 42 | 1.8 | 2793 | 6 | I63351 | I63351 Sequence 5 |
| 1040 | 42 | 1.8 | 2793 | 14 | NPHEGT | M22619 Autographa |
| 1041 | 42 | 1.8 | 14613 | 14 | NPHCUECDYS | M96361 Autographa |
| c1042 | 42 | 1.8 | 40324 | 6 | AX458634 | AX458634 Sequence |
| 1043 | 42 | 1.8 | 50000 | 6 | BD187788 | BD187788 A virus i |
| c1044 | 42 | 1.8 | 67884 | 2 | AC115103 | AC115103 Homo sapi |
| 1045 | 42 | 1.8 | 117951 | 9 | AC023049 | AC023049 Homo sapi |
| c1046 | 42 | 1.8 | 119217 | 14 | AF499596 | AF499596 Phthorima |
| 1047 | 42 | 1.8 | 128413 | 14 | NPHT3COMP | L33180 Bombyx mori |
| 1048 | 42 | 1.8 | 133894 | 6 | A48542 | A48542 Sequence 1 |
| 1049 | 42 | 1.8 | 133894 | 14 | L22858 | L22858 Autographa |
| 1050 | 42 | 1.8 | 149955 | 14 | AY077832 | AY077832 Sheeppox |
| 1051 | 42 | 1.8 | 150158 | 8 | AC136905 | AC136905 Oryza sat |
| 1052 | 42 | 1.8 | 154298 | 8 | AP003504 | AP003504 Oryza sat |
| 1053 | 42 | 1.8 | 156514 | 8 | AP003514 | AP003514 Oryza sat |
| 1054 | 42 | 1.8 | 174183 | 2 | AC149689 | AC149689 Bos tauru |
| 1055 | 42 | 1.8 | 174500 | 8 | AP004738 | AP004738 Oryza sat |
| 1056 | 42 | 1.8 | 182726 | 2 | AC084436 | AC084436 Homo sapi |
| 1057 | 42 | 1.8 | 185592 | 10 | AL773522 | AL773522 Mouse DNA |
| 1058 | 42 | 1.8 | 320135 | 2 | AC151850 | AC151850 Takifugu |
| c1059 | 41.8 | 1.8 | 424 | 6 | AR495496 | AR495496 Sequence |
| c1060 | 41.8 | 1.8 | 424 | 6 | AR510778 | AR510778 Sequence |
| 1061 | 41.8 | 1.8 | 1218 | 6 | CQ801246 | CQ801246 Sequence |
| 1062 | 41.8 | 1.8 | 1457 | 8 | AF127218 | AF127218 Forsythia |
| 1063 | 41.8 | 1.8 | 1470 | 6 | CQ804574 | CQ804574 Sequence |
| 1064 | 41.8 | 1.8 | 1470 | 8 | BT008765 | BT008765 Arabidops |
| 1065 | 41.8 | 1.8 | 1605 | 8 | AY081339 | AY081339 Arabidops |
| 1066 | 41.8 | 1.8 | 2043 | 8 | AB013598 | AB013598 Verbena h |
| 1067 | 41.8 | 1.8 | 2326 | 8 | HVBRNZ1H | X15694 Barley bron |
| 1068 | 41.8 | 1.8 | 6174 | 6 | CQ801273 | CQ801273 Sequence |
| 1069 | 41.8 | 1.8 | 10325 | 6 | CQ801245 | CQ801245 Sequence |
| 1070 | 41.8 | 1.8 | 12134 | 6 | CQ801279 | CQ801279 Sequence |
| c1071 | 41.8 | 1.8 | 50436 | 9 | AL391258 | AL391258 Human DNA |
| 1072 | 41.8 | 1.8 | 57121 | 2 | AC084255 | AC084255 Homo sapi |
| 1073 | 41.8 | 1.8 | 82139 | 3 | AC115684 | AC115684 Dictyoste |
| c1074 | 41.8 | 1.8 | 97681 | 9 | AL138931 | AL138931 Human DNA |
| 1075 | 41.8 | 1.8 | 107200 | 8 | AC006551 | AC006551 Arabidops |
| 1076 | 41.8 | 1.8 | 109873 | 8 | AP003872 | AP003872 Oryza sat |
| c1077 | 41.8 | 1.8 | 115248 | 5 | BX255908 | BX255908 Zebrafish |
| c1078 | 41.8 | 1.8 | 131158 | 14 | AY327402 | AY327402 Choriston |
| 1079 | 41.8 | 1.8 | 148544 | 8 | AP004636 | AP004636 Oryza sat |
| c1080 | 41.8 | 1.8 | 177320 | 2 | AL356777 | AL356777 Homo sapi |
| c1081 | 41.8 | 1.8 | 192867 | 9 | AL358815 | AL358815 Human DNA |
| 1082 | 41.8 | 1.8 | 194693 | 2 | CR753837 | CR753837 Danio rer |
| c1083 | 41.8 | 1.8 | 233688 | 2 | BX571949 | BX571949 Danio rer |
| 1084 | 41.6 | 1.8 | 466 | 6 | AR495991 | AR495991 Sequence |
| 1085 | 41.6 | 1.8 | 466 | 6 | AR511273 | AR511273 Sequence |
| 1086 | 41.6 | 1.8 | 700 | 8 | AY201033 | AY201033 Arabidops |

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|-------|------|-----|--------|----|-----------|--------------------|
| 1087 | 41.6 | 1.8 | 1323 | 6 | AX653753 | AX653753 Sequence |
| 1088 | 41.6 | 1.8 | 1480 | 8 | AK118988 | AK118988 Arabidops |
| 1089 | 41.6 | 1.8 | 7238 | 6 | AX345350 | AX345350 Sequence |
| 1090 | 41.6 | 1.8 | 103517 | 8 | AC073395 | AC073395 Arabidops |
| 1091 | 41.6 | 1.8 | 117296 | 8 | AC008153 | AC008153 Arabidops |
| 1092 | 41.6 | 1.8 | 125283 | 8 | AC144345 | AC144345 Medicago |
| c1093 | 41.6 | 1.8 | 125623 | 3 | AC115599 | AC115599 Dictyoste |
| 1094 | 41.6 | 1.8 | 167628 | 9 | AC092570 | AC092570 Homo sapi |
| c1095 | 41.6 | 1.8 | 197679 | 10 | AC087801 | AC087801 Mus muscu |
| 1096 | 41.6 | 1.8 | 207945 | 10 | AC123945 | AC123945 Mus muscu |
| 1097 | 41.6 | 1.8 | 211456 | 10 | AL928926 | AL928926 Mouse DNA |
| c1098 | 41.6 | 1.8 | 219293 | 2 | AC141471 | AC141471 Mus muscu |
| 1099 | 41.4 | 1.8 | 281 | 8 | NTA538414 | AJ538414 Nicotiana |
| 1100 | 41.4 | 1.8 | 468 | 11 | BV008994 | BV008994 MASC_STSl |
| 1101 | 41.4 | 1.8 | 525 | 11 | BV009008 | BV009008 MASC_STSl |
| 1102 | 41.4 | 1.8 | 1381 | 8 | BT005494 | BT005494 Arabidops |
| 1103 | 41.4 | 1.8 | 1434 | 6 | AX211619 | AX211619 Sequence |
| 1104 | 41.4 | 1.8 | 1507 | 8 | AY084687 | AY084687 Arabidops |
| 1105 | 41.4 | 1.8 | 1584 | 8 | AK071127 | AK071127 Oryza sat |
| 1106 | 41.4 | 1.8 | 1618 | 8 | BT004159 | BT004159 Arabidops |
| 1107 | 41.4 | 1.8 | 37329 | 3 | U97009 | U97009 Caenorhabdi |
| 1108 | 41.4 | 1.8 | 38951 | 3 | CEAC3 | Z71177 Caenorhabdi |
| 1109 | 41.4 | 1.8 | 45701 | 9 | AC099412 | AC099412 Homo sapi |
| 1110 | 41.4 | 1.8 | 45868 | 8 | AC145456 | AC145456 Cicer ari |
| c1111 | 41.4 | 1.8 | 75125 | 8 | AB025604 | AB025604 Arabidops |
| 1112 | 41.4 | 1.8 | 138870 | 8 | AP005659 | AP005659 Oryza sat |
| 1113 | 41.4 | 1.8 | 145988 | 2 | AC024059 | AC024059 Homo sapi |
| c1114 | 41.4 | 1.8 | 161586 | 9 | AC090179 | AC090179 Homo sapi |
| c1115 | 41.4 | 1.8 | 181991 | 2 | AC068322 | AC068322 Homo sapi |
| 1116 | 41.4 | 1.8 | 195806 | 9 | AC027243 | AC027243 Homo sapi |
| c1117 | 41.4 | 1.8 | 215251 | 2 | AC105505 | AC105505 Rattus no |
| 1118 | 41.4 | 1.8 | 236880 | 2 | AC125831 | AC125831 Rattus no |
| 1119 | 41.4 | 1.8 | 248489 | 2 | AC095253 | AC095253 Rattus no |
| 1120 | 41.2 | 1.8 | 1374 | 6 | CQ805414 | CQ805414 Sequence |
| 1121 | 41.2 | 1.8 | 1374 | 6 | AX506881 | AX506881 Sequence |
| 1122 | 41.2 | 1.8 | 1374 | 6 | AX651852 | AX651852 Sequence |
| 1123 | 41.2 | 1.8 | 1405 | 8 | AY117218 | AY117218 Arabidops |
| 1124 | 41.2 | 1.8 | 1617 | 8 | AY056277 | AY056277 Arabidops |
| 1125 | 41.2 | 1.8 | 1732 | 8 | AK099055 | AK099055 Oryza sat |
| 1126 | 41.2 | 1.8 | 1785 | 8 | AK071953 | AK071953 Oryza sat |
| 1127 | 41.2 | 1.8 | 4686 | 6 | AX654735 | AX654735 Sequence |
| 1128 | 41.2 | 1.8 | 7829 | 6 | AX251889 | AX251889 Sequence |
| 1129 | 41.2 | 1.8 | 7829 | 6 | AX344283 | AX344283 Sequence |
| 1130 | 41.2 | 1.8 | 7829 | 6 | AX346007 | AX346007 Sequence |
| 1131 | 41.2 | 1.8 | 7829 | 6 | AX348698 | AX348698 Sequence |
| c1132 | 41.2 | 1.8 | 10710 | 6 | AX345795 | AX345795 Sequence |
| c1133 | 41.2 | 1.8 | 14284 | 14 | AF439352 | AF439352 Choriston |
| 1134 | 41.2 | 1.8 | 24768 | 3 | CET07C5 | Z50006 Caenorhabdi |
| c1135 | 41.2 | 1.8 | 100665 | 8 | AC006533 | AC006533 Arabidops |
| c1136 | 41.2 | 1.8 | 112065 | 8 | AC109596 | AC109596 Oryza sat |
| c1137 | 41.2 | 1.8 | 124131 | 2 | AC016335 | AC016335 Homo sapi |
| 1138 | 41.2 | 1.8 | 128755 | 9 | AC013587 | AC013587 Homo sapi |
| 1139 | 41.2 | 1.8 | 129564 | 9 | AC087302 | AC087302 Homo sapi |
| c1140 | 41.2 | 1.8 | 133352 | 8 | AC108499 | AC108499 Oryza sat |
| c1141 | 41.2 | 1.8 | 138717 | 10 | AL929416 | AL929416 Mouse DNA |
| 1142 | 41.2 | 1.8 | 159891 | 8 | AP004864 | AP004864 Oryza sat |
| 1143 | 41.2 | 1.8 | 161624 | 2 | AP001493 | AP001493 Homo sapi |

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|-------|------|-----|--------|----|-----------|--------------------|-------------|
| c1144 | 41.2 | 1.8 | 167580 | 2 | AC146124 | AC146124 | Pan trogl |
| c1145 | 41.2 | 1.8 | 167932 | 2 | AC068133 | AC068133 | Homo sapi |
| c1146 | 41.2 | 1.8 | 170270 | 2 | AP001548 | AP001548 | Homo sapi |
| 1147 | 41.2 | 1.8 | 170413 | 2 | AC090405 | AC090405 | Homo sapi |
| c1148 | 41.2 | 1.8 | 172655 | 2 | AC104203 | AC104203 | Mus muscu |
| c1149 | 41.2 | 1.8 | 174463 | 5 | BX511007 | BX511007 | Zebrafish |
| 1150 | 41.2 | 1.8 | 174645 | 9 | AC091111 | AC091111 | Homo sapi |
| 1151 | 41.2 | 1.8 | 175850 | 2 | AP001399 | AP001399 | Homo sapi |
| 1152 | 41.2 | 1.8 | 180915 | 8 | GTAJ10592 | AJ010592 | Guillard |
| 1153 | 41.2 | 1.8 | 186150 | 2 | AP001544 | AP001544 | Homo sapi |
| 1154 | 41.2 | 1.8 | 188800 | 2 | AC015846 | AC015846 | Homo sapi |
| c1155 | 41.2 | 1.8 | 194487 | 2 | AP002896 | AP002896 | Homo sapi |
| c1156 | 41.2 | 1.8 | 202699 | 2 | BS000628 | BS000628 | Pan trogl |
| c1157 | 41.2 | 1.8 | 204120 | 8 | AY661659 | AY661659 | Sorghum b |
| 1158 | 41.2 | 1.8 | 204340 | 9 | AC091103 | AC091103 | Homo sapi |
| 1159 | 41.2 | 1.8 | 209710 | 9 | CNS01DXF | AL139296 | Human chr |
| 1160 | 41.2 | 1.8 | 230714 | 9 | AC147345 | AC147345 | Pan trogl |
| 1161 | 41.2 | 1.8 | 271793 | 2 | BX572620 | BX572620 | Danio rer |
| c1162 | 41.2 | 1.8 | 291421 | 2 | AC132939 | AC132939 | Mus muscu |
| 1163 | 41 | 1.8 | 1423 | 8 | AY519364 | AY519364 | Citrus si |
| 1164 | 41 | 1.8 | 1479 | 6 | AX653930 | AX653930 | Sequence |
| 1165 | 41 | 1.8 | 2000 | 6 | AX656007 | AX656007 | Sequence |
| 1166 | 41 | 1.8 | 2111 | 14 | AF000009 | AF000009 | Heliothis |
| c1167 | 41 | 1.8 | 110000 | 2 | CR388160 | Continuation (2 of | |
| c1168 | 41 | 1.8 | 135507 | 9 | AL590733 | AL590733 | Human DNA |
| 1169 | 41 | 1.8 | 146885 | 2 | BX957322 | BX957322 | Danio rer |
| 1170 | 41 | 1.8 | 159419 | 5 | AC144823 | AC144823 | Danio rer |
| c1171 | 41 | 1.8 | 162134 | 2 | AC022478 | AC022478 | Homo sapi |
| 1172 | 41 | 1.8 | 172614 | 9 | AL929302 | AL929302 | Human DNA |
| 1173 | 41 | 1.8 | 173411 | 9 | AC092754 | AC092754 | Homo sapi |
| 1174 | 41 | 1.8 | 176202 | 9 | CNS05TF3 | AL359951 | Human chr |
| 1175 | 41 | 1.8 | 187429 | 9 | AC092755 | AC092755 | Homo sapi |
| c1176 | 41 | 1.8 | 208770 | 2 | CR388155 | CR388155 | Danio rer |
| 1177 | 41 | 1.8 | 216567 | 2 | BX927074 | BX927074 | Danio rer |
| 1178 | 41 | 1.8 | 229637 | 2 | CR556716 | CR556716 | Danio rer |
| 1179 | 40.8 | 1.8 | 1361 | 8 | AB070749 | AB070749 | Vigna ang |
| 1180 | 40.8 | 1.8 | 1398 | 6 | AX653340 | AX653340 | Sequence |
| 1181 | 40.8 | 1.8 | 1415 | 8 | MECGT1 | X77459 | M.esculenta |
| c1182 | 40.8 | 1.8 | 1581 | 8 | AK120020 | AK120020 | Oryza sat |
| 1183 | 40.8 | 1.8 | 1586 | 8 | AK064270 | AK064270 | Oryza sat |
| 1184 | 40.8 | 1.8 | 1656 | 8 | AK068040 | AK068040 | Oryza sat |
| c1185 | 40.8 | 1.8 | 1706 | 8 | AK108055 | AK108055 | Oryza sat |
| 1186 | 40.8 | 1.8 | 1962 | 8 | AK063325 | AK063325 | Oryza sat |
| c1187 | 40.8 | 1.8 | 7554 | 3 | AY160096 | AY160096 | Dictyoste |
| c1188 | 40.8 | 1.8 | 16841 | 9 | AB044136 | AB044136 | Homo sapi |
| 1189 | 40.8 | 1.8 | 36846 | 2 | AC149390 | AC149390 | Phakopsor |
| c1190 | 40.8 | 1.8 | 59940 | 2 | AC024414 | AC024414 | Homo sapi |
| 1191 | 40.8 | 1.8 | 70204 | 9 | AC010737 | AC010737 | Homo sapi |
| 1192 | 40.8 | 1.8 | 77204 | 8 | AB046438 | AB046438 | Arabidops |
| c1193 | 40.8 | 1.8 | 84705 | 3 | CEY48E1B | Z93393 | Caenorhabdi |
| 1194 | 40.8 | 1.8 | 97352 | 8 | AC091670 | AC091670 | Oryza sat |
| 1195 | 40.8 | 1.8 | 102230 | 8 | AP004045 | AP004045 | Oryza sat |
| c1196 | 40.8 | 1.8 | 121501 | 8 | AC069557 | AC069557 | Genomic S |
| 1197 | 40.8 | 1.8 | 132558 | 3 | AC025716 | AC025716 | Caenorhab |
| c1198 | 40.8 | 1.8 | 133476 | 9 | AC008804 | AC008804 | Homo sapi |
| c1199 | 40.8 | 1.8 | 133889 | 8 | AC133334 | AC133334 | Oryza sat |
| c1200 | 40.8 | 1.8 | 149972 | 2 | AC101817 | AC101817 | Mus muscu |

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|-------|------|-----|--------|----|-------------|--------------------|
| 1201 | 40.8 | 1.8 | 153297 | 2 | AC027558 | AC027558 Homo sapi |
| 1202 | 40.8 | 1.8 | 178376 | 8 | AP005008 | AP005008 Oryza sat |
| c1203 | 40.8 | 1.8 | 190666 | 2 | AY245865 | AY245865 Homo sapi |
| 1204 | 40.8 | 1.8 | 198845 | 5 | BX510333 | BX510333 Zebrafish |
| 1205 | 40.8 | 1.8 | 203595 | 2 | CR385054 | CR385054 Danio rer |
| 1206 | 40.8 | 1.8 | 247275 | 10 | AC100736 | AC100736 Mus muscu |
| c1207 | 40.8 | 1.8 | 274626 | 2 | AC006903 | AC006903 Caenorhab |
| 1208 | 40.8 | 1.8 | 340801 | 2 | AC006751 | AC006751 Caenorhab |
| c1209 | 40.8 | 1.8 | 348174 | 3 | CR382399 | CR382399 Plasmodiu |
| c1210 | 40.8 | 1.8 | 349960 | 6 | AX573241 | AX573241 Sequence |
| 1211 | 40.6 | 1.8 | 1768 | 8 | AB098614 | AB098614 Glycyrrhi |
| 1212 | 40.6 | 1.8 | 6325 | 3 | DDI012088 | AJ012088 Dictyoste |
| 1213 | 40.6 | 1.8 | 38206 | 9 | AL356984 | AL356984 Human DNA |
| c1214 | 40.6 | 1.8 | 110000 | 2 | PFMAL13_04 | Continuation (5 of |
| c1215 | 40.6 | 1.8 | 143291 | 9 | HS163G9 | AL008733 Human DNA |
| c1216 | 40.6 | 1.8 | 173223 | 9 | AP003777 | AP003777 Homo sapi |
| 1217 | 40.6 | 1.8 | 214480 | 2 | AC113517 | AC113517 Mus muscu |
| 1218 | 40.6 | 1.8 | 222186 | 2 | AC120362 | AC120362 Mus muscu |
| 1219 | 40.6 | 1.8 | 257258 | 2 | AC105322 | AC105322 Mus muscu |
| 1220 | 40.6 | 1.8 | 293431 | 2 | PFMAL13P4 | AL049181 Plasmodiu |
| 1221 | 40.6 | 1.8 | 349980 | 6 | AX344551 | AX344551 Sequence |
| 1222 | 40.4 | 1.7 | 404 | 3 | MAU42338 | U42338 Meloidogyne |
| 1223 | 40.4 | 1.7 | 1293 | 8 | BT011794 | BT011794 Arabidops |
| 1224 | 40.4 | 1.7 | 1437 | 6 | AX652925 | AX652925 Sequence |
| 1225 | 40.4 | 1.7 | 1440 | 6 | AX766278 | AX766278 Sequence |
| 1226 | 40.4 | 1.7 | 1514 | 8 | AK110876 | AK110876 Oryza sat |
| 1227 | 40.4 | 1.7 | 1537 | 8 | CAR400861 | AJ400861 Cicer ari |
| 1228 | 40.4 | 1.7 | 1567 | 8 | AY625694 | AY625694 Oryza sat |
| 1229 | 40.4 | 1.7 | 1664 | 8 | AK061830 | AK061830 Oryza sat |
| 1230 | 40.4 | 1.7 | 1686 | 8 | AK102335 | AK102335 Oryza sat |
| 1231 | 40.4 | 1.7 | 1725 | 8 | AK064351 | AK064351 Oryza sat |
| 1232 | 40.4 | 1.7 | 1779 | 8 | AK102415 | AK102415 Oryza sat |
| c1233 | 40.4 | 1.7 | 59793 | 8 | AB025634 | AB025634 Arabidops |
| 1234 | 40.4 | 1.7 | 110000 | 2 | PFMAL8P1_11 | Continuation (12 o |
| 1235 | 40.4 | 1.7 | 132254 | 3 | AC116330 | AC116330 Dictyoste |
| 1236 | 40.4 | 1.7 | 157987 | 8 | AP003560 | AP003560 Oryza sat |
| 1237 | 40.4 | 1.7 | 211799 | 2 | AC138229 | AC138229 Mus muscu |
| 1238 | 40.4 | 1.7 | 226627 | 2 | AC134181 | AC134181 Rattus no |
| c1239 | 40.4 | 1.7 | 230926 | 2 | AC114457 | AC114457 Rattus no |
| 1240 | 40.4 | 1.7 | 348034 | 3 | CR382400 | CR382400 Plasmodiu |
| c1241 | 40.2 | 1.7 | 366 | 1 | AY430162 | AY430162 Helicobac |
| c1242 | 40.2 | 1.7 | 366 | 1 | AY430163 | AY430163 Helicobac |
| c1243 | 40.2 | 1.7 | 366 | 1 | AY430165 | AY430165 Helicobac |
| c1244 | 40.2 | 1.7 | 805 | 11 | BV026811 | BV026811 S212P6802 |
| 1245 | 40.2 | 1.7 | 863 | 8 | HVU496572 | AJ496572 Hordeum v |
| 1246 | 40.2 | 1.7 | 1383 | 6 | CQ806198 | CQ806198 Sequence |
| 1247 | 40.2 | 1.7 | 1399 | 8 | AY128739 | AY128739 Arabidops |
| 1248 | 40.2 | 1.7 | 1402 | 8 | AY133752 | AY133752 Arabidops |
| 1249 | 40.2 | 1.7 | 1418 | 8 | AY114654 | AY114654 Arabidops |
| 1250 | 40.2 | 1.7 | 1426 | 8 | AY072325 | AY072325 Arabidops |
| 1251 | 40.2 | 1.7 | 1492 | 8 | AY062589 | AY062589 Arabidops |
| 1252 | 40.2 | 1.7 | 1565 | 8 | AY074526 | AY074526 Arabidops |
| 1253 | 40.2 | 1.7 | 1640 | 8 | AK105783 | AK105783 Oryza sat |
| 1254 | 40.2 | 1.7 | 1665 | 8 | AK105966 | AK105966 Oryza sat |
| 1255 | 40.2 | 1.7 | 1673 | 8 | AK119530 | AK119530 Oryza sat |
| 1256 | 40.2 | 1.7 | 36075 | 3 | AF025468 | AF025468 Caenorhab |
| c1257 | 40.2 | 1.7 | 96123 | 9 | AC114311 | AC114311 Homo sapi |

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|-------|------|-----|--------|----|------------|--------------------|
| c1258 | 40.2 | 1.7 | 98101 | 8 | ATF2K13 | AL391141 Arabidops |
| 1259 | 40.2 | 1.7 | 104305 | 8 | AC140022 | AC140022 Medicago |
| 1260 | 40.2 | 1.7 | 107014 | 8 | OSJN00218 | AL663021 Oryza sat |
| c1261 | 40.2 | 1.7 | 107014 | 8 | OSJN00218 | AL663021 Oryza sat |
| 1262 | 40.2 | 1.7 | 108530 | 5 | BX247884 | BX247884 Zebrafish |
| 1263 | 40.2 | 1.7 | 109918 | 9 | AC114279 | AC114279 Homo sapi |
| c1264 | 40.2 | 1.7 | 110000 | 2 | AC115142_0 | AC115142 Rattus no |
| c1265 | 40.2 | 1.7 | 123500 | 14 | U53466 | U53466 Cydia pomon |
| c1266 | 40.2 | 1.7 | 129563 | 8 | OSJN00008 | AL606443 Oryza sat |
| c1267 | 40.2 | 1.7 | 140691 | 9 | AF159056 | AF159056 Homo sapi |
| 1268 | 40.2 | 1.7 | 143036 | 2 | AC015498 | AC015498 Homo sapi |
| c1269 | 40.2 | 1.7 | 143205 | 8 | AC093018 | AC093018 Oryza sat |
| 1270 | 40.2 | 1.7 | 145427 | 5 | BX276112 | BX276112 Zebrafish |
| 1271 | 40.2 | 1.7 | 149662 | 14 | AY077834 | AY077834 Sheeppox |
| 1272 | 40.2 | 1.7 | 150057 | 14 | AY077833 | AY077833 Sheeppox |
| 1273 | 40.2 | 1.7 | 152009 | 2 | AC010802 | AC010802 Homo sapi |
| c1274 | 40.2 | 1.7 | 156814 | 8 | AP005004 | AP005004 Oryza sat |
| 1275 | 40.2 | 1.7 | 162281 | 9 | AC105395 | AC105395 Homo sapi |
| 1276 | 40.2 | 1.7 | 171816 | 9 | AC006033 | AC006033 Homo sapi |
| 1277 | 40.2 | 1.7 | 171926 | 2 | AC144073 | AC144073 Macaca mu |
| 1278 | 40.2 | 1.7 | 173218 | 2 | AP004686 | AP004686 Oryza sat |
| 1279 | 40.2 | 1.7 | 173219 | 2 | BX897738 | BX897738 Danio rer |
| c1280 | 40.2 | 1.7 | 189631 | 2 | AC009920 | AC009920 Homo sapi |
| c1281 | 40.2 | 1.7 | 191935 | 2 | AC114747 | AC114747 Homo sapi |
| c1282 | 40.2 | 1.7 | 198944 | 8 | ATCHRIV38 | AL161538 Arabidops |
| c1283 | 40.2 | 1.7 | 199138 | 2 | CR450798 | CR450798 Danio rer |
| c1284 | 40.2 | 1.7 | 200576 | 8 | ATFCA0 | Z97335 Arabidopsis |
| 1285 | 40.2 | 1.7 | 203114 | 2 | AC011818 | AC011818 Homo sapi |
| c1286 | 40.2 | 1.7 | 229726 | 2 | AC109699 | AC109699 Rattus no |
| 1287 | 40.2 | 1.7 | 235614 | 2 | CR450721 | CR450721 Danio rer |
| c1288 | 40.2 | 1.7 | 280915 | 2 | AC112104 | AC112104 Rattus no |
| 1289 | 40.2 | 1.7 | 349980 | 6 | AX344566 | AX344566 Sequence |
| 1290 | 40 | 1.7 | 1219 | 8 | AK068336 | AK068336 Oryza sat |
| 1291 | 40 | 1.7 | 1350 | 6 | AX653931 | AX653931 Sequence |
| 1292 | 40 | 1.7 | 1377 | 8 | BT002638 | BT002638 Arabidops |
| 1293 | 40 | 1.7 | 1411 | 8 | BT000356 | BT000356 Arabidops |
| 1294 | 40 | 1.7 | 1457 | 6 | AX211618 | AX211618 Sequence |
| 1295 | 40 | 1.7 | 1562 | 8 | AY120731 | AY120731 Arabidops |
| 1296 | 40 | 1.7 | 1572 | 8 | AY048297 | AY048297 Arabidops |
| 1297 | 40 | 1.7 | 1661 | 8 | AK105967 | AK105967 Oryza sat |
| 1298 | 40 | 1.7 | 1686 | 8 | AK060997 | AK060997 Oryza sat |
| 1299 | 40 | 1.7 | 1696 | 8 | AK103242 | AK103242 Oryza sat |
| 1300 | 40 | 1.7 | 1842 | 8 | AK106302 | AK106302 Oryza sat |
| c1301 | 40 | 1.7 | 2026 | 8 | AK117305 | AK117305 Arabidops |
| 1302 | 40 | 1.7 | 6029 | 6 | AX346895 | AX346895 Sequence |
| 1303 | 40 | 1.7 | 7631 | 6 | AX345762 | AX345762 Sequence |
| 1304 | 40 | 1.7 | 8576 | 6 | AX347130 | AX347130 Sequence |
| 1305 | 40 | 1.7 | 10716 | 6 | AX346320 | AX346320 Sequence |
| c1306 | 40 | 1.7 | 11985 | 9 | BX322534 | BX322534 Human DNA |
| 1307 | 40 | 1.7 | 17389 | 6 | AX346316 | AX346316 Sequence |
| 1308 | 40 | 1.7 | 27332 | 3 | CER11A8 | Z70310 Caenorhabdi |
| 1309 | 40 | 1.7 | 34548 | 6 | AX349036 | AX349036 Sequence |
| 1310 | 40 | 1.7 | 84985 | 1 | SNA278573 | AJ278573 Streptomy |
| 1311 | 40 | 1.7 | 94555 | 9 | AL589684 | AL589684 Human DNA |
| 1312 | 40 | 1.7 | 97033 | 2 | AC015146 | AC015146 Drosophil |
| c1313 | 40 | 1.7 | 100815 | 8 | ATF12A12 | AL133314 Arabidops |
| 1314 | 40 | 1.7 | 104071 | 2 | AL162260 | AL162260 Homo sapi |

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|-------|------|-----|--------|----|-------------|--------------------|
| 1315 | 40 | 1.7 | 110000 | 2 | AC120698_0 | AC120698 Rattus no |
| 1316 | 40 | 1.7 | 110000 | 2 | AC120698_1 | Continuation (2 of |
| c1317 | 40 | 1.7 | 110000 | 2 | BX276116_07 | Continuation (8 of |
| c1318 | 40 | 1.7 | 110000 | 2 | BX276116_08 | Continuation (9 of |
| 1319 | 40 | 1.7 | 110000 | 3 | AC116984_1 | Continuation (2 of |
| 1320 | 40 | 1.7 | 143508 | 9 | HSJ570L12 | AL049589 Human DNA |
| 1321 | 40 | 1.7 | 160366 | 3 | AC069457 | AC069457 Drosophil |
| 1322 | 40 | 1.7 | 160776 | 2 | AC137960 | AC137960 Mus muscu |
| 1323 | 40 | 1.7 | 168438 | 2 | AC024632 | AC024632 Homo sapi |
| 1324 | 40 | 1.7 | 168953 | 9 | AL360219 | AL360219 Human DNA |
| c1325 | 40 | 1.7 | 178433 | 9 | CNS01RHH | AL161752 Human chr |
| 1326 | 40 | 1.7 | 180574 | 9 | AC092807 | AC092807 Homo sapi |
| 1327 | 40 | 1.7 | 181927 | 3 | AC010573 | AC010573 Drosophil |
| c1328 | 40 | 1.7 | 182963 | 2 | AC116815 | AC116815 Mus muscu |
| c1329 | 40 | 1.7 | 184470 | 9 | AL589823 | AL589823 Human DNA |
| c1330 | 40 | 1.7 | 220897 | 2 | AL954635 | AL954635 Homo sapi |
| c1331 | 40 | 1.7 | 226142 | 2 | AC126422 | AC126422 Mus muscu |
| c1332 | 40 | 1.7 | 243348 | 2 | AC150646 | AC150646 Bos tauru |
| 1333 | 40 | 1.7 | 246640 | 2 | AC108286 | AC108286 Rattus no |
| c1334 | 40 | 1.7 | 265352 | 2 | AC095748 | AC095748 Rattus no |
| 1335 | 40 | 1.7 | 278708 | 3 | AE003535 | AE003535 Drosophil |
| c1336 | 40 | 1.7 | 300050 | 1 | AP004171 | AP004171 Mycoplasm |
| 1337 | 40 | 1.7 | 349980 | 6 | AX344552 | AX344552 Sequence |
| c1338 | 39.8 | 1.7 | 289 | 6 | AR162089 | AR162089 Sequence |
| c1339 | 39.8 | 1.7 | 289 | 6 | AR166614 | AR166614 Sequence |
| 1340 | 39.8 | 1.7 | 993 | 8 | MECGT7 | X77464 M.esculenta |
| 1341 | 39.8 | 1.7 | 1371 | 6 | AX412848 | AX412848 Sequence |
| 1342 | 39.8 | 1.7 | 1371 | 6 | AX506822 | AX506822 Sequence |
| 1343 | 39.8 | 1.7 | 1371 | 6 | AX766276 | AX766276 Sequence |
| 1344 | 39.8 | 1.7 | 1371 | 8 | BT000622 | BT000622 Arabidops |
| 1345 | 39.8 | 1.7 | 1371 | 8 | BT005368 | BT005368 Arabidops |
| 1346 | 39.8 | 1.7 | 1407 | 6 | AX653241 | AX653241 Sequence |
| 1347 | 39.8 | 1.7 | 1437 | 6 | AX211638 | AX211638 Sequence |
| c1348 | 39.8 | 1.7 | 1437 | 6 | AX211640 | AX211640 Sequence |
| 1349 | 39.8 | 1.7 | 1451 | 6 | AX211616 | AX211616 Sequence |
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| c1358 | 39.8 | 1.7 | 11086 | 1 | AE010596 | AE010596 Fusobacte |
| 1359 | 39.8 | 1.7 | 60193 | 9 | AL359705 | AL359705 Human DNA |
| c1360 | 39.8 | 1.7 | 73184 | 2 | AC090864 | AC090864 Homo sapi |
| c1361 | 39.8 | 1.7 | 79991 | 2 | AC108505 | AC108505 Oryza sat |
| c1362 | 39.8 | 1.7 | 87637 | 9 | AL390960 | AL390960 Human DNA |
| c1363 | 39.8 | 1.7 | 104001 | 8 | AC023628 | AC023628 Arabidops |
| 1364 | 39.8 | 1.7 | 107139 | 2 | AL360223 | AL360223 Homo sapi |
| 1365 | 39.8 | 1.7 | 108881 | 8 | AC002391 | AC002391 Arabidops |
| 1366 | 39.8 | 1.7 | 109659 | 2 | AC151499 | AC151499 Dasypus n |
| c1367 | 39.8 | 1.7 | 110000 | 2 | AC116234_1 | Continuation (2 of |
| 1368 | 39.8 | 1.7 | 118584 | 14 | AY043265 | AY043265 Epiphyas |
| 1369 | 39.8 | 1.7 | 124186 | 9 | AL772392 | AL772392 Human DNA |
| 1370 | 39.8 | 1.7 | 144572 | 5 | BX322794 | BX322794 Zebrafish |
| 1371 | 39.8 | 1.7 | 146782 | 2 | AC127599 | AC127599 Rattus no |

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| c1372 | 39.8 | 1.7 | 153576 | 2 | AC020572 | AC020572 | Homo sapi |
| 1373 | 39.8 | 1.7 | 162605 | 2 | AC068698 | AC068698 | Homo sapi |
| c1374 | 39.8 | 1.7 | 163088 | 9 | AC097654 | AC097654 | Homo sapi |
| 1375 | 39.8 | 1.7 | 163364 | 2 | AC116241 | AC116241 | Rattus no |
| c1376 | 39.8 | 1.7 | 180005 | 2 | AC136070 | AC136070 | Rattus no |
| c1377 | 39.8 | 1.7 | 187651 | 8 | AC129718 | AC129718 | Oryza sat |
| c1378 | 39.8 | 1.7 | 189139 | 2 | AC122947 | AC122947 | Rattus no |
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| 1380 | 39.8 | 1.7 | 201427 | 2 | AC127843 | AC127843 | Rattus no |
| c1381 | 39.8 | 1.7 | 213678 | 2 | AC137173 | AC137173 | Rattus no |
| c1382 | 39.8 | 1.7 | 215675 | 2 | AC123264 | AC123264 | Rattus no |
| c1383 | 39.8 | 1.7 | 220283 | 2 | AC103391 | AC103391 | Mus muscu |
| c1384 | 39.8 | 1.7 | 221631 | 9 | AC010867 | AC010867 | Homo sapi |
| c1385 | 39.8 | 1.7 | 224818 | 2 | AC111839 | AC111839 | Rattus no |
| c1386 | 39.8 | 1.7 | 231770 | 2 | AC109171 | AC109171 | Mus muscu |
| 1387 | 39.8 | 1.7 | 238637 | 2 | AC092254 | AC092254 | Mus muscu |
| 1388 | 39.8 | 1.7 | 245515 | 2 | AC151275 | AC151275 | Mus muscu |
| 1389 | 39.8 | 1.7 | 245795 | 2 | AC096419 | AC096419 | Rattus no |
| 1390 | 39.8 | 1.7 | 249487 | 2 | AC095161 | AC095161 | Rattus no |
| 1391 | 39.8 | 1.7 | 250178 | 2 | AC118121 | AC118121 | Rattus no |
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| c1396 | 39.8 | 1.7 | 299467 | 2 | AC120784 | AC120784 | Mus muscu |
| 1397 | 39.6 | 1.7 | 1231 | 1 | AY234840 | AY234840 | Staphyloc |
| 1398 | 39.6 | 1.7 | 1368 | 14 | AF166115 | AF166115 | Potato vi |
| 1399 | 39.6 | 1.7 | 1387 | 8 | AY117336 | AY117336 | Arabidops |
| 1400 | 39.6 | 1.7 | 1419 | 6 | AX653260 | AX653260 | Sequence |
| 1401 | 39.6 | 1.7 | 1433 | 6 | AX211617 | AX211617 | Sequence |
| 1402 | 39.6 | 1.7 | 1443 | 14 | PVYDNA0 | Z50042 | Potato viru |
| 1403 | 39.6 | 1.7 | 1443 | 14 | PVYDNA1 | Z50041 | Potato viru |
| 1404 | 39.6 | 1.7 | 1443 | 14 | PVYDNAONA | Z50043 | Potato viru |
| 1405 | 39.6 | 1.7 | 1596 | 8 | AY084880 | AY084880 | Arabidops |
| 1406 | 39.6 | 1.7 | 1689 | 8 | AY080716 | AY080716 | Arabidops |
| 1407 | 39.6 | 1.7 | 1980 | 14 | BSU61154 | U61154 | Buzura supp |
| c1408 | 39.6 | 1.7 | 5858 | 3 | AF350276 | AF350276 | Nephila m |
| 1409 | 39.6 | 1.7 | 6104 | 6 | AX346269 | AX346269 | Sequence |
| c1410 | 39.6 | 1.7 | 8004 | 6 | CQ588884 | CQ588884 | Sequence |
| 1411 | 39.6 | 1.7 | 8033 | 3 | PPINMP | Y13117 | Paramecium |
| c1412 | 39.6 | 1.7 | 8736 | 6 | CQ588875 | CQ588875 | Sequence |
| 1413 | 39.6 | 1.7 | 9958 | 3 | AF246689 | AF246689 | Dictyoste |
| 1414 | 39.6 | 1.7 | 12500 | 3 | AF482381 | AF482381 | Dictyoste |
| 1415 | 39.6 | 1.7 | 15052 | 1 | AF055579 | AF055579 | Streptomy |
| c1416 | 39.6 | 1.7 | 34919 | 3 | AF100663 | AF100663 | Caenorhab |
| c1417 | 39.6 | 1.7 | 37225 | 9 | AC005954 | AC005954 | Homo sapi |
| 1418 | 39.6 | 1.7 | 49817 | 2 | AC013939 | AC013939 | Drosophil |
| 1419 | 39.6 | 1.7 | 50937 | 6 | AR159871 | AR159871 | Sequence |
| c1420 | 39.6 | 1.7 | 53920 | 9 | AC116423 | AC116423 | Homo sapi |
| 1421 | 39.6 | 1.7 | 71225 | 9 | AL358196 | AL358196 | Human DNA |
| 1422 | 39.6 | 1.7 | 74492 | 8 | AY350713 | AY350713 | Capsella |
| c1423 | 39.6 | 1.7 | 83528 | 8 | AP005695 | AP005695 | Oryza sat |
| c1424 | 39.6 | 1.7 | 85916 | 3 | AC117080 | AC117080 | Dictyoste |
| c1425 | 39.6 | 1.7 | 103908 | 2 | AC150245 | AC150245 | Medicago |
| c1426 | 39.6 | 1.7 | 128018 | 2 | BX890615 | BX890615 | Danio rer |
| c1427 | 39.6 | 1.7 | 138158 | 5 | BX005232 | BX005232 | Zebrafish |
| 1428 | 39.6 | 1.7 | 139147 | 2 | AC006725 | AC006725 | Caenorhab |

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| c1429 | 39.6 | 1.7 | 148397 | 2 | CR751563 | CR751563 | Danio rer |
| 1430 | 39.6 | 1.7 | 150876 | 2 | AC108761 | AC108761 | Oryza sat |
| 1431 | 39.6 | 1.7 | 154082 | 2 | AC108756 | AC108756 | Oryza sat |
| c1432 | 39.6 | 1.7 | 154195 | 2 | AC013641 | AC013641 | Homo sapi |
| c1433 | 39.6 | 1.7 | 167195 | 3 | AC007808 | AC007808 | Drosophil |
| 1434 | 39.6 | 1.7 | 170425 | 5 | BX465867 | BX465867 | Zebrafish |
| 1435 | 39.6 | 1.7 | 179399 | 5 | AL929338 | AL929338 | Zebrafish |
| c1436 | 39.6 | 1.7 | 185672 | 2 | BX640474 | BX640474 | Danio rer |
| 1437 | 39.6 | 1.7 | 187495 | 9 | AC026887 | AC026887 | Homo sapi |
| 1438 | 39.6 | 1.7 | 188638 | 2 | CR759889 | CR759889 | Danio rer |
| 1439 | 39.6 | 1.7 | 210700 | 2 | AC103382 | AC103382 | Mus muscu |
| 1440 | 39.6 | 1.7 | 212134 | 2 | AC024037 | AC024037 | Homo sapi |
| 1441 | 39.6 | 1.7 | 212499 | 2 | CR626887 | CR626887 | Danio rer |
| c1442 | 39.6 | 1.7 | 215210 | 2 | CR749744 | CR749744 | Danio rer |
| 1443 | 39.6 | 1.7 | 219892 | 2 | AC127200 | AC127200 | Rattus no |
| 1444 | 39.6 | 1.7 | 220817 | 2 | AC113854 | AC113854 | Rattus no |
| 1445 | 39.6 | 1.7 | 226092 | 2 | AC107090 | AC107090 | Rattus no |
| c1446 | 39.6 | 1.7 | 233220 | 2 | AC098058 | AC098058 | Rattus no |
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| 1448 | 39.6 | 1.7 | 254733 | 3 | AC117075 | AC117075 | Dictyoste |
| c1449 | 39.6 | 1.7 | 254961 | 3 | AE003706 | AE003706 | Drosophil |
| 1450 | 39.6 | 1.7 | 269863 | 2 | AC131017 | AC131017 | Rattus no |
| 1451 | 39.4 | 1.7 | 640 | 6 | AX652149 | AX652149 | Sequence |
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| 1454 | 39.4 | 1.7 | 1479 | 8 | AB191246 | AB191246 | Dianthus |
| 1455 | 39.4 | 1.7 | 1918 | 8 | AK102481 | AK102481 | Oryza sat |
| c1456 | 39.4 | 1.7 | 1921 | 6 | CQ577878 | CQ577878 | Sequence |
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| c1458 | 39.4 | 1.7 | 2534 | 3 | BT001649 | BT001649 | Drosophil |
| 1459 | 39.4 | 1.7 | 4141 | 6 | CQ577877 | CQ577877 | Sequence |
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| 1461 | 39.4 | 1.7 | 11155 | 6 | AX345507 | AX345507 | Sequence |
| c1462 | 39.4 | 1.7 | 38801 | 3 | CEK09B11 | Z83114 | Caenorhabdi |
| c1463 | 39.4 | 1.7 | 39329 | 9 | AC004091 | AC004091 | Human Cos |
| c1464 | 39.4 | 1.7 | 43644 | 9 | AC004092 | AC004092 | Human Cos |
| 1465 | 39.4 | 1.7 | 47108 | 6 | AX344507 | AX344507 | Sequence |
| c1466 | 39.4 | 1.7 | 60220 | 3 | AC115604 | AC115604 | Dictyoste |
| c1467 | 39.4 | 1.7 | 74630 | 9 | AL157903 | AL157903 | Human DNA |
| c1468 | 39.4 | 1.7 | 87501 | 8 | CR380951_6 | Continuation (7 of | |
| c1469 | 39.4 | 1.7 | 99699 | 2 | AC013845 | AC013845 | Drosophil |
| c1470 | 39.4 | 1.7 | 117099 | 8 | AP003572 | AP003572 | Oryza sat |
| c1471 | 39.4 | 1.7 | 127131 | 8 | AC146819 | AC146819 | Medicago |
| c1472 | 39.4 | 1.7 | 128223 | 8 | AP005643 | AP005643 | Oryza sat |
| c1473 | 39.4 | 1.7 | 131734 | 2 | CR792420 | CR792420 | Danio rer |
| 1474 | 39.4 | 1.7 | 136471 | 8 | AP003622 | AP003622 | Oryza sat |
| 1475 | 39.4 | 1.7 | 138850 | 8 | AC133341 | AC133341 | Medicago |
| 1476 | 39.4 | 1.7 | 140757 | 9 | AL157778 | AL157778 | Human DNA |
| c1477 | 39.4 | 1.7 | 144022 | 5 | BX088594 | BX088594 | Zebrafish |
| c1478 | 39.4 | 1.7 | 147245 | 8 | AP003217 | AP003217 | Oryza sat |
| 1479 | 39.4 | 1.7 | 147640 | 2 | AP003542 | AP003542 | Oryza sat |
| 1480 | 39.4 | 1.7 | 155906 | 8 | AP005934 | AP005934 | Oryza sat |
| c1481 | 39.4 | 1.7 | 160285 | 2 | CR848001 | CR848001 | Danio rer |
| 1482 | 39.4 | 1.7 | 168269 | 2 | CR352217 | CR352217 | Danio rer |
| 1483 | 39.4 | 1.7 | 171165 | 2 | CR376767 | CR376767 | Danio rer |
| 1484 | 39.4 | 1.7 | 172854 | 3 | AC023706 | AC023706 | Drosophil |
| c1485 | 39.4 | 1.7 | 175947 | 8 | AP003435 | AP003435 | Oryza sat |

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| 1486 | 39.4 | 1.7 | 177743 | 9 | AC105941 | AC105941 Homo sapi |
| c1487 | 39.4 | 1.7 | 183648 | 3 | AC117081 | AC117081 Dictyoste |
| c1488 | 39.4 | 1.7 | 186739 | 9 | AC072028 | AC072028 Homo sapi |
| 1489 | 39.4 | 1.7 | 189441 | 2 | AC022989 | AC022989 Homo sapi |
| c1490 | 39.4 | 1.7 | 190930 | 2 | BX936353 | BX936353 Danio rer |
| 1491 | 39.4 | 1.7 | 191590 | 3 | AC023722 | AC023722 Drosophil |
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| 1493 | 39.4 | 1.7 | 197419 | 8 | ATCHRIV41 | AL161541 Arabidops |
| 1494 | 39.4 | 1.7 | 198019 | 5 | BX469910 | BX469910 Zebrafish |
| 1495 | 39.4 | 1.7 | 198946 | 10 | AL844548 | AL844548 Mouse DNA |
| 1496 | 39.4 | 1.7 | 200252 | 8 | ATFCA3 | Z97338 Arabidopsis |
| c1497 | 39.4 | 1.7 | 205225 | 2 | CR812896 | CR812896 Danio rer |
| 1498 | 39.4 | 1.7 | 216131 | 5 | BX005004 | BX005004 Zebrafish |
| c1499 | 39.4 | 1.7 | 224731 | 2 | AC105545 | AC105545 Rattus no |
| 1500 | 39.4 | 1.7 | 273275 | 3 | AE014828 | AE014828 Plasmodiu |

ALIGNMENTS

RESULT 1

AX697213

LOCUS AX697213 2320 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 281 from Patent WO0078961.

ACCESSION AX697213

VERSION AX697213.1 GI:29498151

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L., Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0078961-A 281 28-DEC-2000; Genentech Inc. (US)

FEATURES Location/Qualifiers

source 1. .2320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2320; DB 6; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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| | | | |
|----|-----|---|-----|
| Db | 61 | AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT | 120 |
| Qy | 121 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 180 |
| Db | 121 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 180 |
| Qy | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 240 |
| Db | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 240 |
| Qy | 241 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG | 300 |
| Db | 241 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG | 300 |
| Qy | 301 | TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 360 |
| Db | 301 | TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 360 |
| Qy | 361 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
| Db | 361 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 480 |
| Db | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 480 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| Db | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| Qy | 541 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC | 600 |
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| Qy | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC | 780 |
| Db | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC | 780 |
| Qy | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
| Db | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
| Qy | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
| Db | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
| Qy | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 960 |
| Db | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 960 |

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| Qy | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
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| Db | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
| Qy | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTTCATTGGCCCAA | 1080 |
| | | | |
| Db | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTTCATTGGCCCAA | 1080 |
| Qy | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
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| Db | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
| Qy | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| | | | |
| Db | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| Qy | 1201 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1260 |
| | | | |
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| Qy | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTAGTTAAAGAAGCTCAAGGCAGA | 1320 |
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| Db | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTAGTTAAAGAAGCTCAAGGCAGA | 1320 |
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| | | | |
| Db | 1501 | GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1560 |
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| | | | |
| Db | 1561 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1620 |
| Qy | 1621 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1680 |
| | | | |
| Db | 1621 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1680 |
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| Db | 1681 | TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1740 |
| Qy | 1741 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA | 1800 |
| | | | |
| Db | 1741 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA | 1800 |

Qy 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
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 Db 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860

Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
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 Db 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Db 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980

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Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 2

AY358416

LOCUS AY358416 2320 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA71169 glucuronosyltransferase (UNQ842) mRNA, complete cds.

ACCESSION AY358416

VERSION AY358416.1 GI:37181956

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2320)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,

Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 2320)
 AUTHORS Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 2320; DB 9; Length 2320;
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 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | |
| Db | 1 | AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA | 60 |
| Qy | 61 | AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT | 120 |
| | | | |
| Db | 61 | AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT | 120 |
| Qy | 121 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 180 |
| | | | |
| Db | 121 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 180 |
| Qy | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 240 |
| | | | |

| | | | |
|----|------|---|------|
| Db | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 240 |
| Qy | 241 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG | 300 |
| | | | |
| Db | 241 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG | 300 |
| Qy | 301 | TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 360 |
| | | | |
| Db | 301 | TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 360 |
| Qy | 361 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
| | | | |
| Db | 361 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 480 |
| | | | |
| Db | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 480 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| | | | |
| Db | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| Qy | 541 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC | 600 |
| | | | |
| Db | 541 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC | 600 |
| Qy | 601 | AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 660 |
| | | | |
| Db | 601 | AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 660 |
| Qy | 661 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 720 |
| | | | |
| Db | 661 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 720 |
| Qy | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC | 780 |
| | | | |
| Db | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC | 780 |
| Qy | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
| | | | |
| Db | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
| Qy | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
| | | | |
| Db | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
| Qy | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT | 960 |
| | | | |
| Db | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT | 960 |
| Qy | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
| | | | |
| Db | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
| Qy | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA | 1080 |
| | | | |
| Db | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA | 1080 |

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| Qy | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
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| Db | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
| Qy | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| | | | |
| Db | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| Qy | 1201 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1260 |
| | | | |
| Db | 1201 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1260 |
| Qy | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1320 |
| | | | |
| Db | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1320 |
| Qy | 1321 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1380 |
| | | | |
| Db | 1321 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1380 |
| Qy | 1381 | GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1440 |
| | | | |
| Db | 1381 | GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1440 |
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| | | | |
| Db | 1441 | GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA | 1500 |
| Qy | 1501 | GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1560 |
| | | | |
| Db | 1501 | GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1560 |
| Qy | 1561 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1620 |
| | | | |
| Db | 1561 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1620 |
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| | | | |
| Db | 1621 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1680 |
| Qy | 1681 | TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1740 |
| | | | |
| Db | 1681 | TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1740 |
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| | | | |
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| Qy | 1861 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 1920 |
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| Db | 1861 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 1920 |

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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RESULT 3

AX136141

LOCUS AX136141 2341 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 63 from Patent EP1067182.

ACCESSION AX136141

VERSION AX136141.1 GI:14272549

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 63 10-JAN-2001;

Helix Research Institute (JP)

FEATURES

Location/Qualifiers

source

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ORIGIN

Query Match 99.6%; Score 2310.2; DB 6; Length 2341;
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| Db | 147 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 206 |
| Qy | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTACCATTGCTTAACCA | 240 |
| | | | |
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| Qy | 241 | CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG | 300 |
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| Qy | 301 | TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGTATTCTTTCTGGA | 360 |
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| Qy | 361 | AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
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| Db | 387 | AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 446 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA | 480 |
| | | | |
| Db | 447 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA | 506 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| | | | |
| Db | 507 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 566 |
| Qy | 541 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC | 600 |
| | | | |
| Db | 567 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC | 626 |
| Qy | 601 | AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCCTTGCTGACTGATCACATGGACTTCTG | 660 |
| | | | |

| | | | |
|----|------|---|------|
| Db | 627 | AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG | 686 |
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| | | | |
| Db | 687 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 746 |
| Qy | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC | 780 |
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| Qy | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
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| Db | 807 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 866 |
| Qy | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
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| Db | 867 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 926 |
| Qy | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 960 |
| | | | |
| Db | 927 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 986 |
| Qy | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
| | | | |
| Db | 987 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1046 |
| Qy | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA | 1080 |
| | | | |
| Db | 1047 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA | 1106 |
| Qy | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
| | | | |
| Db | 1107 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1166 |
| Qy | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| | | | |
| Db | 1167 | GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1226 |
| Qy | 1201 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1260 |
| | | | |
| Db | 1227 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1286 |
| Qy | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTCAGTTAAAGAAGCTCAAGGCAGA | 1320 |
| | | | |
| Db | 1287 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTCAGTTAAAGAAGCTCAAGGCAGA | 1346 |
| Qy | 1321 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1380 |
| | | | |
| Db | 1347 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1406 |
| Qy | 1381 | GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1440 |
| | | | |
| Db | 1407 | GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1466 |
| Qy | 1441 | GATTGACCACGTCTTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTTACGCA | 1500 |
| | | | |
| Db | 1467 | GATTGACCACGTCTTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTTACGCA | 1526 |

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|----|------|---|------|
| Qy | 1501 | GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1560 |
| | | | |
| Db | 1527 | GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1586 |
| Qy | 1561 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1620 |
| | | | |
| Db | 1587 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1646 |
| Qy | 1621 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1680 |
| | | | |
| Db | 1647 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1706 |
| Qy | 1681 | TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1740 |
| | | | |
| Db | 1707 | TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1766 |
| Qy | 1741 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA | 1800 |
| | | | |
| Db | 1767 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA | 1826 |
| Qy | 1801 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT | 1860 |
| | | | |
| Db | 1827 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT | 1886 |
| Qy | 1861 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 1920 |
| | | | |
| Db | 1887 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 1946 |
| Qy | 1921 | TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC | 1980 |
| | | | |
| Db | 1947 | TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC | 2006 |
| Qy | 1981 | CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC | 2040 |
| | | | |
| Db | 2007 | CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC | 2066 |
| Qy | 2041 | TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT | 2100 |
| | | | |
| Db | 2067 | TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT | 2126 |
| Qy | 2101 | TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG | 2160 |
| | | | |
| Db | 2127 | TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG | 2186 |
| Qy | 2161 | AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA | 2220 |
| | | | |
| Db | 2187 | AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA | 2246 |
| Qy | 2221 | CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA | 2280 |
| | | | |
| Db | 2247 | CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA | 2306 |
| Qy | 2281 | AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC | 2315 |
| | | | |
| Db | 2307 | AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC | 2341 |

RESULT 4

BD123523

LOCUS BD123523 2341 bp DNA linear PAT 18-SEP-2002

DEFINITION Secretory protein or membrane protein.

ACCESSION BD123523

VERSION BD123523.1 GI:23218468

KEYWORDS JP 2002017376-A/32.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2341)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: JP 2002017376-A 32 22-JAN-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002017376-A/32

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU

PI SUGIYAMA,

PI KOJI HAYASHI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ 10, PC

C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC

Secretory protein or membrane protein

FH Key Location/Qualifiers

FT CDS (94)..(1662).

FEATURES Location/Qualifiers

source

1..2341

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 99.6%; Score 2310.2; DB 6; Length 2341;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
          |||
Db      27 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 86

Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
          |||
Db      87 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 146

Qy     121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
          |||
Db     147 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 206

Qy     181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
          |||

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| | | | |
|----|------|---|------|
| Db | 207 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 266 |
| Qy | 241 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG | 300 |
| | | | |
| Db | 267 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG | 326 |
| Qy | 301 | TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 360 |
| | | | |
| Db | 327 | TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 386 |
| Qy | 361 | AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
| | | | |
| Db | 387 | AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 446 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 480 |
| | | | |
| Db | 447 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 506 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| | | | |
| Db | 507 | CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 566 |
| Qy | 541 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC | 600 |
| | | | |
| Db | 567 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC | 626 |
| Qy | 601 | AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 660 |
| | | | |
| Db | 627 | AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 686 |
| Qy | 661 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 720 |
| | | | |
| Db | 687 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 746 |
| Qy | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCT | 780 |
| | | | |
| Db | 747 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCT | 806 |
| Qy | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
| | | | |
| Db | 807 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 866 |
| Qy | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
| | | | |
| Db | 867 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 926 |
| Qy | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 960 |
| | | | |
| Db | 927 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 986 |
| Qy | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
| | | | |
| Db | 987 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1046 |
| Qy | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA | 1080 |
| | | | |
| Db | 1047 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA | 1106 |

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| Qy | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
| | | | |
| Db | 1107 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1166 |
| Qy | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTCACCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| | | | |
| Db | 1167 | GGCTCACCCAAGCATCCGTCTGTTTGTCACCACGGCGGGCAGAATAGCATAATGGAGGC | 1226 |
| Qy | 1201 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1260 |
| | | | |
| Db | 1227 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1286 |
| Qy | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1320 |
| | | | |
| Db | 1287 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1346 |
| Qy | 1321 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1380 |
| | | | |
| Db | 1347 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1406 |
| Qy | 1381 | GGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1440 |
| | | | |
| Db | 1407 | GGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1466 |
| Qy | 1441 | GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA | 1500 |
| | | | |
| Db | 1467 | GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA | 1526 |
| Qy | 1501 | GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1560 |
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| Db | 1527 | GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1586 |
| Qy | 1561 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1620 |
| | | | |
| Db | 1587 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1646 |
| Qy | 1621 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1680 |
| | | | |
| Db | 1647 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1706 |
| Qy | 1681 | TCACCATTCTAGGGAGCTTCCCAGTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1740 |
| | | | |
| Db | 1707 | TCACCATTCTAGGGAGCTTCCCAGTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1766 |
| Qy | 1741 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA | 1800 |
| | | | |
| Db | 1767 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA | 1826 |
| Qy | 1801 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT | 1860 |
| | | | |
| Db | 1827 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT | 1886 |
| Qy | 1861 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA | 1920 |
| | | | |
| Db | 1887 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA | 1946 |

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Db 1947 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 2006
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 Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
 |||
 Db 2007 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2066
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 Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
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 Db 2067 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2126
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 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2127 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2186
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 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 |||
 Db 2247 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2306
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 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCAACCTC 2315
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RESULT 5

AK075383

LOCUS AK075383 2341 bp mRNA linear PRI 03-SEP-2002
 DEFINITION Homo sapiens cDNA PSEC0073 fis, clone NT2RP2002934, weakly similar to UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17).

ACCESSION AK075383

VERSION AK075383.1 GI:22761433

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
 AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2341)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University

of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES

source

Location/Qualifiers

1. .2341

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/mol_type="mRNA"

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/clone="NT2RP2002934"

/cell_line="NT2"

/cell_type="teratocarcinoma"

/clone_lib="NT2RP2"

/note="cloning vector: pME18SFL3~mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

CDS

94. .1665

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HWPVKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVGIPLFG
DQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAVAASVILRSHPLS
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ORIGIN

Query Match 99.6%; Score 2310.2; DB 9; Length 2341;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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| Qy | 1 | AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA | 60 |
| | | | |
| Db | 27 | AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA | 86 |
| Qy | 61 | AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGCGGCTTCCTTCTCCCTGGGGTCCCT | 120 |
| | | | |
| Db | 87 | AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGCGGCTTCCTTCTCCCTGGGGTCCCT | 146 |
| Qy | 121 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 180 |
| | | | |
| Db | 147 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 206 |
| Qy | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 240 |
| | | | |
| Db | 207 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 266 |
| Qy | 241 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG | 300 |
| | | | |
| Db | 267 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG | 326 |
| Qy | 301 | TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 360 |
| | | | |
| Db | 327 | TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 386 |

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|----|------|---|------|
| Qy | 361 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
| | | | |
| Db | 387 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 446 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTTCCTTAAAGAATGAGAA | 480 |
| | | | |
| Db | 447 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTTCCTTAAAGAATGAGAA | 506 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| | | | |
| Db | 507 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 566 |
| Qy | 541 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC | 600 |
| | | | |
| Db | 567 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC | 626 |
| Qy | 601 | AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 660 |
| | | | |
| Db | 627 | AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 686 |
| Qy | 661 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 720 |
| | | | |
| Db | 687 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 746 |
| Qy | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC | 780 |
| | | | |
| Db | 747 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC | 806 |
| Qy | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
| | | | |
| Db | 807 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 866 |
| Qy | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
| | | | |
| Db | 867 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 926 |
| Qy | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT | 960 |
| | | | |
| Db | 927 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT | 986 |
| Qy | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
| | | | |
| Db | 987 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1046 |
| Qy | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA | 1080 |
| | | | |
| Db | 1047 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA | 1106 |
| Qy | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
| | | | |
| Db | 1107 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1166 |
| Qy | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| | | | |
| Db | 1167 | GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1226 |

| | | | |
|----|------|---|------|
| Qy | 1201 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1260 |
| | | | |
| Db | 1227 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1286 |
| Qy | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1320 |
| | | | |
| Db | 1287 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1346 |
| Qy | 1321 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1380 |
| | | | |
| Db | 1347 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1406 |
| Qy | 1381 | GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1440 |
| | | | |
| Db | 1407 | GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1466 |
| Qy | 1441 | GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA | 1500 |
| | | | |
| Db | 1467 | GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA | 1526 |
| Qy | 1501 | GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1560 |
| | | | |
| Db | 1527 | GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1586 |
| Qy | 1561 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1620 |
| | | | |
| Db | 1587 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1646 |
| Qy | 1621 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1680 |
| | | | |
| Db | 1647 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1706 |
| Qy | 1681 | TCACCATTTCTAGGGAGCTTCCCAGTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1740 |
| | | | |
| Db | 1707 | TCACCATTTCTAGGGAGCTTCCCAGTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1766 |
| Qy | 1741 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCAGTTGCTA | 1800 |
| | | | |
| Db | 1767 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCAGTTGCTA | 1826 |
| Qy | 1801 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT | 1860 |
| | | | |
| Db | 1827 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT | 1886 |
| Qy | 1861 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 1920 |
| | | | |
| Db | 1887 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 1946 |
| Qy | 1921 | TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC | 1980 |
| | | | |
| Db | 1947 | TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC | 2006 |
| Qy | 1981 | CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC | 2040 |
| | | | |
| Db | 2007 | CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC | 2066 |
| Qy | 2041 | TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTTCTTTCAGT | 2100 |

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Db      2067  TGGCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2126
Qy      2101  TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
Db      2127  TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2186
Qy      2161  AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
Db      2187  AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2246
Qy      2221  CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
Db      2247  CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2306
Qy      2281  AATAAAAGTTTACAGCGTTATCTCTCCCAACCTC 2315
Db      2307  AATAAAAGTTTACAGCGTTATCTCTCCCAACCTC 2341

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RESULT 6

AX548037

LOCUS AX548037 2944 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 13 from Patent WO02066654.

ACCESSION AX548037

VERSION AX548037.1 GI:25813133

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Astromoff,A., Au-Young,J., Baughn,M.R., Ding,L., Duggan,B.M.,
Forsythe,I.J., Gietzen,K.J., Griffin,J.A., Lee,E.A., Lu,Y.,
Richardson,T.W., Ring,H.Z., Sanjanwala,M.M., Swarnakar,A.,
Walia,N.K., Warren,B.A., Xu,Y., Yue,H. and Zebarjadian,Y.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 02066654-A 13 29-AUG-2002;

Incyte Genomics, Inc. (US)

FEATURES

Location/Qualifiers

source

1. .2944

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="Incyte ID No: 7486594CB1"

ORIGIN

Query Match

90.6%; Score 2102.8; DB 6; Length 2944;

Best Local Similarity 95.5%; Pred. No. 0;

Matches 2216; Conservative 0; Mismatches 2; Indels 102; Gaps 1;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Db 204 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 263

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCCT 120

| | | | |
|----|------|---|------|
| Db | 264 | AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT | 323 |
| Qy | 121 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT | 180 |
| Db | 324 | GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGT----- | 362 |
| Qy | 181 | GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA | 240 |
| Db | 363 | ----- | 362 |
| Qy | 241 | CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG | 300 |
| Db | 363 | -----AGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG | 401 |
| Qy | 301 | TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 360 |
| Db | 402 | TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA | 461 |
| Qy | 361 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 420 |
| Db | 462 | AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC | 521 |
| Qy | 421 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 480 |
| Db | 522 | GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA | 581 |
| Qy | 481 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 540 |
| Db | 582 | CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT | 641 |
| Qy | 541 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACC | 600 |
| Db | 642 | TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACC | 701 |
| Qy | 601 | AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 660 |
| Db | 702 | AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG | 761 |
| Qy | 661 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 720 |
| Db | 762 | GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA | 821 |
| Qy | 721 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC | 780 |
| Db | 822 | GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC | 881 |
| Qy | 781 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 840 |
| Db | 882 | TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC | 941 |
| Qy | 841 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 900 |
| Db | 942 | TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC | 1001 |
| Qy | 901 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 960 |
| Db | 1002 | AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT | 1061 |

| | | | |
|----|------|---|------|
| Qy | 961 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1020 |
| | | | |
| Db | 1062 | GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA | 1121 |
| Qy | 1021 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAA | 1080 |
| | | | |
| Db | 1122 | TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAA | 1181 |
| Qy | 1081 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1140 |
| | | | |
| Db | 1182 | AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT | 1241 |
| Qy | 1141 | GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1200 |
| | | | |
| Db | 1242 | GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC | 1301 |
| Qy | 1201 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1260 |
| | | | |
| Db | 1302 | CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT | 1361 |
| Qy | 1261 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1320 |
| | | | |
| Db | 1362 | GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA | 1421 |
| Qy | 1321 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1380 |
| | | | |
| Db | 1422 | GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT | 1481 |
| Qy | 1381 | GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1440 |
| | | | |
| Db | 1482 | GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG | 1541 |
| Qy | 1441 | GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA | 1500 |
| | | | |
| Db | 1542 | GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA | 1601 |
| Qy | 1501 | GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1560 |
| | | | |
| Db | 1602 | GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG | 1661 |
| Qy | 1561 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1620 |
| | | | |
| Db | 1662 | GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG | 1721 |
| Qy | 1621 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1680 |
| | | | |
| Db | 1722 | AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG | 1781 |
| Qy | 1681 | TCACCATTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1740 |
| | | | |
| Db | 1782 | TCACCATTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT | 1841 |
| Qy | 1741 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA | 1800 |
| | | | |
| Db | 1842 | TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA | 1901 |

| | | | |
|----|------|--|------|
| Qy | 1801 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT | 1860 |
| | | | |
| Db | 1902 | ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT | 1961 |
| Qy | 1861 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 1920 |
| | | | |
| Db | 1962 | CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT | 2021 |
| Qy | 1921 | TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC | 1980 |
| | | | |
| Db | 2022 | TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC | 2081 |
| Qy | 1981 | CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC | 2040 |
| | | | |
| Db | 2082 | CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC | 2141 |
| Qy | 2041 | TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT | 2100 |
| | | | |
| Db | 2142 | TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT | 2201 |
| Qy | 2101 | TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG | 2160 |
| | | | |
| Db | 2202 | TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG | 2261 |
| Qy | 2161 | AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA | 2220 |
| | | | |
| Db | 2262 | AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA | 2321 |
| Qy | 2221 | CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA | 2280 |
| | | | |
| Db | 2322 | CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA | 2381 |
| Qy | 2281 | AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA | 2320 |
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| Db | 2382 | AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA | 2421 |

RESULT 7

AX958403

LOCUS AX958403 2263 bp DNA linear PAT 14-JAN-2004

DEFINITION Sequence 31 from Patent WO0226988.

ACCESSION AX958403

VERSION AX958403.1 GI:40879361

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS

TITLE Human drug metabolizing enzymes

JOURNAL Patent: WO 0226988-A 31 04-APR-2002;

Incyte Genomics, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .2263

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 68.1%; Score 1578.8; DB 6; Length 2263;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1658; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

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Qy      7 CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAG 66
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Db     22 CCTTAGCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAG 81

Qy     67 CATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGTCTCTC 126
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Db     82 CATGGTTGGGCAGCGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCTGTCTCTC 141

Qy    127 AGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA 186
        |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  ||||  ||||
Db    142 AGAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGA 201

Qy    187 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG 246
        |||||  |||||||  ||||  |||||||  |||||||  |||||||  ||||  ||||  ||
Db    202 CCGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGG 261

Qy    247 AGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCT 306
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Db    262 AAAGTTTTTGTATCCCAGATATTAAAGAGGAGGAAAATCATACCAAGTTATCAGGTGGTT 321

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Db    322 TTCACCTGAAGATCATCAAAAAGAATTAAGAAGCATTTTGATAGCTACATAGAAACAGC 381

Qy    367 TTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCA 426
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Db    382 ATTGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCA 441

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Qy    547 GCCATTTGTGGCCATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACCAATCCC 606
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Qy    607 CTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCG 666
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Db    622 CTTGTCTTATGTTCCAGTATTCCTTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCG 681

Qy    667 AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTAC 726
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Db 982 TGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTT 1041

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Db 1102 CCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA 1161

Qy 1147 CCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCA 1206
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Db 1222 GCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCG 1281

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Db 1282 AGTAGAAGCCAAAAAGTTTGGTGTCTATTAGTTAAAGAAGCTCAAGGCAGAGACATT 1341

Qy 1327 GGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGC 1386
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Qy 1567 ATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGT 1626
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Db 1582 ATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGT 1641

Qy 1627 GAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCA 1686
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 Db 1642 GAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCA 1701
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 Db 1702 TTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTC 1761
 Qy 1747 CTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTT 1796
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 Db 1762 CTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACAT 1811

RESULT 8

AX359921

LOCUS AX359921 2082 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 1 from Patent WO0202774.

ACCESSION AX359921

VERSION AX359921.1 GI:18675563

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Leiby, K.R., Cook, W.J. and Spaltmann, F.

TITLE 32626, a human udp-glycosyltransferase and uses thereof

JOURNAL Patent: WO 0202774-A 1 10-JAN-2002;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .2082

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

CDS

145. .1716

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ORIGIN

Query Match 55.2%; Score 1281.6; DB 6; Length 2082;

Best Local Similarity 85.9%; Pred. No. 0;

Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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| Db | 84 | CCTTAGCCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAG | 143 |
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| Qy | 187 | CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG | 246 |
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| Qy | 247 | AGGTCCTTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCT | 306 |
| Db | 324 | AAAGTTTTTGATCCAGATATTAAGAGGAGGAAAATCATACCAAGTTATCAGGTGGTT | 383 |
| Qy | 307 | TGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAAAC | 366 |
| Db | 384 | TTCACCTGAAGATCATCAAAAAGAATTAAGAAGCATTTTGATAGCTACATAGAAACAGC | 443 |
| Qy | 367 | TTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCA | 426 |
| Db | 444 | ATTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAATATTTGGGACTCA | 503 |
| Qy | 427 | GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGA | 486 |
| Db | 504 | ATGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCTTAAAGAATGAGAACTATGA | 563 |
| Qy | 487 | CATGGTGATAGTTGAAACTTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAA | 546 |
| Db | 564 | TCTGGTATTTGTTGAAGCATTTGATTTCTGTTCTTTCTGATTGCTGAGAAGCTTGTGAA | 623 |
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| Db | 684 | CTTGTCTTATGTTCCAGTATTCCCTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG | 743 |
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| Qy | 787 | TCTACTGAAAGCAGAGTTGTGGTTCAATTAAGCTGACTTTGCCTTTGATTTTGCTCGACC | 846 |
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Db 1044 TGGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCCTCAAGAAGATGCACAATGCCTT 1103

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Db 1164 TCATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA 1223

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LOCUS AX155211 2797 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1 from Patent WO0138505.
 ACCESSION AX155211
 VERSION AX155211.1 GI:14536690
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Adler,D.A., Dong,D.L., Pownder,S., Gao,Z. and Conklin,D.C.
 TITLE Secretd protein, zalpha37
 JOURNAL Patent: WO 0138505-A 1 31-MAY-2001;
 ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers
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ORIGIN

Query Match 55.2%; Score 1281.6; DB 6; Length 2797;
 Best Local Similarity 85.9%; Pred. No. 0;
 Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy 7 CCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAG 66
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 Qy 187 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG 246
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| Db | 418 | ATTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCA | 477 |
| Qy | 427 | GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTTCCTTAAAGAATGAGAACTTCGA | 486 |
| Db | 478 | ATGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTTCCTTAAAGAATGAGAACTATGA | 537 |
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| Qy | 547 | GCCATTTGTGGCCATTCTTTCCACTTCATTCCGCTCTTTGGAATTTGGGCTACCAATCCC | 606 |
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| Qy | 607 | CTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCG | 666 |
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| Db | 718 | AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTAC | 777 |
| Qy | 727 | ATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCT | 786 |
| Db | 778 | ATTTGACAACACCATCAAGGAGCATTCCCAGAAGGCTCTAGGCCAGTTTTGTCTCATCT | 837 |
| Qy | 787 | TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTGACC | 846 |
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| Db | 1018 | TGGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCTCAAGAAGATGCACAATGCCTT | 1077 |
| Qy | 1027 | TGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAGATGT | 1086 |
| Db | 1078 | TGCCCACCTCCCTCAAGGAGTGATATGGACATGTCAGAGTTCTCATTGGCCCAGAGATGT | 1137 |
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Db 1138 TCATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA 1197

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RESULT 10

AX714604

LOCUS AX714604 2823 bp DNA linear PAT 15-APR-2003

DEFINITION Sequence 1288 from Patent EP1293569.

ACCESSION AX714604

VERSION AX714604.1 GI:29889557

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.

TITLE Full-length cDNAs

JOURNAL Patent: EP 1293569-A 1288 19-MAR-2003;

Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)

FEATURES Location/Qualifiers
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ORIGIN

Query Match 55.2%; Score 1281.6; DB 6; Length 2823;
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Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy 1507 GCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCT 1566

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Db      1717 GAAGAAGACATGAGGCTAGGTGTAGCCTTGGGTGAG 1752

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RESULT 11

AK057066

LOCUS AK057066 2823 bp mRNA linear PRI 30-JAN-2004

DEFINITION Homo sapiens cDNA FLJ32504 fis, clone SMINT1000016, weakly similar to 2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR (EC 2.4.1.45).

ACCESSION AK057066

VERSION AK057066.1 GI:16552643

KEYWORDS oligo capping; fis (full insert sequence).

| | |
|--------|----------------------|
| SOURCE | Homo sapiens (human) |
|--------|----------------------|

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Miyasashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.

TITLE

human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED 14702039
REFERENCE 2
AUTHORS Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.
and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2823)
AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
HRI.

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ORIGIN

Query Match 55.2%; Score 1281.6; DB 9; Length 2823;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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| | | | |
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| Db | 97 | CCTTAGCCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAG | 156 |
| Qy | 67 | CATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTCTC | 126 |
| Db | 157 | CATGGTTGGGCAGCGGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCCTGCTCTC | 216 |
| Qy | 127 | AGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA | 186 |
| Db | 217 | AGAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGA | 276 |
| Qy | 187 | CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCACAAAAG | 246 |
| Db | 277 | CCGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGG | 336 |
| Qy | 247 | AGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCT | 306 |
| Db | 337 | AAAGTTTTTGATCCAGATATTAAAGAGGAGGAAAATCATACCAAGTTATCAGGTGGTT | 396 |
| Qy | 307 | TGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAAAC | 366 |
| Db | 397 | TTACCTGAAGATCATCAAAAAAGAATTAAGAAGCATTTTGATAGCTACATAGAAACAGC | 456 |
| Qy | 367 | TTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCA | 426 |
| Db | 457 | ATTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCA | 516 |
| Qy | 427 | GTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGA | 486 |
| Db | 517 | ATGTAGTTATTTTGCTAAGCAGAAAAGGATATAATGGATTCCTTAAAGAATGAGAACTGTGA | 576 |
| Qy | 487 | CATGGTGATAGTTGAAACTTTTGACTACTGTCTTTCTTGATTGCTGAGAAGCTTGGGAA | 546 |
| Db | 577 | TCTGGTATTTGTTGAAGCATTTGATTTCTGTTCTTTCTTGATTGCTGAGAAGCTTGTGAA | 636 |
| Qy | 547 | GCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCC | 606 |
| Db | 637 | ACCATTTGTGGCCATTCTTCCCACCACATTTCGGCTCTTTGGATTTTGGGCTACCAAGCCC | 696 |
| Qy | 607 | CTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG | 666 |
| Db | 697 | CTTGTCTTATGTTCCAGTATTCCCTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCG | 756 |
| Qy | 667 | AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTAC | 726 |
| Db | 757 | AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTAC | 816 |
| Qy | 727 | ATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCT | 786 |
| Db | 817 | ATTTGACAACACCATCAAGGAGCATTTCCAGAAGGCTCTAGGCCAGTTTTGTCTCATCT | 876 |
| Qy | 787 | TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTGACC | 846 |
| Db | 877 | TCTACTGAAAGCAGAGTTGTGGTTTGTAACTCTGATTTTGCCTTTGATTTTGCCGGCC | 936 |
| Qy | 847 | TCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACCAGTACC | 906 |

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Qy 907 ACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTT 966
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Db 1057 TGGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCCTCAAGAAGATGCACAATGCCTT 1116

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Db 1417 GACACTTACAATGAAACAAGTCATAGAAGACAAGAGGTACAAGTCGGCAGTGGTGGCAGC 1476

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Db 1477 CAGTGTCTCCTGCACTCTCAGCCCCTGAGCCCCGCACAGCGGCTGGTGGGCTGGATCGA 1536

Qy 1447 CCACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTTCAGCAGCCCTG 1506
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Db 1537 CCACATCCTCCAGACTGGGGGAGCGACGCACCTCAAGCCCTATGTCTTCCAGCAGCCTTG 1596

Qy 1507 GCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCT 1566
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Db 1597 GCATGAGCAGTACCTCATTGATGTCTTTGTGTTTCTGCTGGGGCTCACTCTGGGCACTAT 1656

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Db 1657 GTGGCTTTGTGGGAAGCTGCTGGGTGTGGTGGCCAGGTGGCTGCGTGGGGCCAGGAAGGT 1716

Qy 1627 GAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGG 1662
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Db 1717 GAAGAAGACATGAGGCTAGGTGTAGCCTTGGGTGAG 1752

LOCUS BC068446 2759 bp mRNA linear PRI 30-JUN-2004
 DEFINITION Homo sapiens hypothetical protein FLJ34658, mRNA (cDNA clone MGC:86988 IMAGE:5295502), complete cds.
 ACCESSION BC068446
 VERSION BC068446.1 GI:46250395
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2759)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2759)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (02-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 168 Row: c Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24432082.

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FEATURES             Location/Qualifiers
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                        /lab_host="DH10B"
                        /note="Vector: pBluescript"
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ORIGIN

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Query Match          55.2%; Score 1280.6; DB 9; Length 2759;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1421; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy      8 CTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGAAGTGAGC 67
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Db      1 CTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAGC 60

Qy     68 ATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTCTCA 127
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Db     61 ATGGTTGGGCAGCGGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCCTGCTCTCA 120

Qy    128 GAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGAC 187
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Qy    188 CGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGA 247
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Qy    248 GGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTT 307
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Qy 308 GCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGAAGAACT 367
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Qy 428 TGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGAC 487
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 Db 421 TGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCCTTAAAGAATGAGAACTATGAT 480

Qy 488 ATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAG 547
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Qy 548 CCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCC 607
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 Db 541 CCATTTGTGGCCATTCTTCCACCACATTCGGCTCTTTGGATTTTGGGCTACCAAGCCCC 600

Qy 608 TTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGA 667
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 Db 601 TTGTCTTATGTTCCAGTATTCCCTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGA 660

Qy 668 GTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACA 727
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Qy 728 TTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTT 787
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 Db 721 TTTGACAACACCATCAAGGAGCATTTCAGGAAGGCTCTAGGCCAGTTTTGTCTCATCTT 780

Qy 788 CTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTCCTTTGATTTTGTCTCGACCT 847
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 Db 781 CTACTGAAAGCAGAGTTGTGGTTTGTAACTCTGATTTTGCCTTTGATTTTGCCTGGGCC 840

Qy 848 CTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCA 907
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 Db 841 CTGCTTCCCAACACTGTTTATATTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCA 900

Qy 908 CAAGACTTGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTG 967
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 Db 901 CAAGACTTGAGAACTTCATTGCCAAGTTTGGGGATGCAGGGTTTGTCTTGTGGCCTTT 960

Qy 968 GGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT 1027
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 Db 961 GGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCTCAAGAAGATGCACAATGCCTTT 1020

Qy 1028 GCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAAGATGTC 1087
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 Db 1021 GCCCACCTCCCTCAAGGAGTGATATGGACATGTGAGAGTTCTCATTGGCCCAGAGATGTT 1080

Qy 1088 CACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC 1147
 |||||
 Db 1081 CATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC 1140

| | | | |
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| Qy | 1148 | CCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG | 1207 |
| Db | 1141 | CCCAGCATCCGTCTTTTTGTCACTCATGGTGGGCAGAACAGCGTAATGGAGGCCATCCGT | 1200 |
| Qy | 1208 | CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA | 1267 |
| Db | 1201 | CATGGTGTGCCCATGGTGGGATTACCAGTCAATGGAGACCAGCATGAAACATGGTCCGA | 1260 |
| Qy | 1268 | GTAGAAGCCAAAAAGTTTGGTGTCTTCTATTCACTTAAAGAAGCTCAAGGCAGAGACATTG | 1327 |
| Db | 1261 | GTAGTAGCCAAAAATTATGGTGTCTCTATCCGGTTGAATCAGGTCACAGCCGACACACTG | 1320 |
| Qy | 1328 | GCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCC | 1387 |
| Db | 1321 | ACACTTACAATGAAACAAGTCATAGAAGACAAGAGGTACAAGTCGGCAGTGGTGGCAGCC | 1380 |
| Qy | 1388 | AGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGAC | 1447 |
| Db | 1381 | AGTGTTCATCCTGCACTCTCAGCCCCTGAGCCCCGCACAGCGGCTGGTGGGCTGGATCGAC | 1440 |
| Qy | 1448 | CACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCAGCCCTGG | 1507 |
| Db | 1441 | CACATCCTCCAGACTGGGGGAGCGACGCACCTCAAGCCCTATGCCTTCCAGCAGCCTTGG | 1500 |
| Qy | 1508 | CATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA | 1567 |
| Db | 1501 | CATGAGCAGTACCTCATTGATGTCTTTGTGTTTCTGCTGGGGCTCACTCTGGGCATATG | 1560 |
| Qy | 1568 | TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG | 1627 |
| Db | 1561 | TGGCTTTGTGGGAAGCTGCTGGGTGTGGTGGCCAGGTGGCTGCGTGGGGCCAGGAAGGTG | 1620 |
| Qy | 1628 | AAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGG | 1662 |
| Db | 1621 | AAGAAGACATGAGGCTAGGTGTAGCCTTGGGTGAG | 1655 |

RESULT 13

AX327327

LOCUS AX327327 2086 bp DNA linear PAT 07-JAN-2002

DEFINITION Sequence 12 from Patent WO0179468.

ACCESSION AX327327

VERSION AX327327.1 GI:18097873

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Policky, J. L., Hafalia, A., Burford, N., Ring, H. Z., Lal, P., Tribouley, C. M., Yao, M. G., Yue, H., Tang, Y. T., Patterson, C., Das, D., Sanjanwala, M. S., Gandhi, A. R., Reddy, R., Khan, F. A., Baughn, M. R., Ramkumar, J., Griffin, J. A. and Au-Young, J.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 0179468-A 12 25-OCT-2001;
Incyte Genomics, Inc. (US)

FEATURES Location/Qualifiers

source 1. .2086
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 2516747CB1"

ORIGIN

Query Match 55.2%; Score 1280; DB 6; Length 2086;
Best Local Similarity 85.8%; Pred. No. 0;
Matches 1421; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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Qy      7 CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAG 66
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Db      59 CCTTAGCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAG 118

Qy      67 CATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGTCTCTC 126
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Qy     187 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG 246
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Db     299 AAAGTTTTTGTATCCCAGATATTAAAGAGGAGGAAAATCATACCAAGTTATCAGGTGGTT 358

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Qy     367 TTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCA 426
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Qy     487 CATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCCTGATTGCTGAGAAGCTTGGGAA 546
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Db     599 ACCATTTGTGGCCATTCTTCCACCACATTCCGGCTCTTTGGATTTTGGGCTACCAAGCCC 658

Qy     607 CTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG 666
        ||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     659 CTTGTCTTATGTTCCAGTATTCCCTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCG 718

Qy     667 AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTAC 726
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Db 719 AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTAC 778

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Db 839 TCTACTGAAAGCAGAGTTGTGGTTTGTTAACCTCTGATTTTGCCTTTGATTTTGCCCGGCC 898

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Db 899 CCTGCTTCCCAACACTGTTTATATTGGAGGCTTGATGGAAAAACCTATTAACACAGTACC 958

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Db 959 ACAAGACTTGGACAACCTTCATTGCCAACCTTGGGGATGCAGGGTTTGTCTTGTGGCCTT 1018

Qy 967 GGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTT 1026
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Db 1019 TGGCTCCATGTTGAACACCCATCAGTCCAGGAAGTCCCTCAAGAAGATGCACAATGCCTT 1078

Qy 1027 TGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAAGATGT 1086
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Db 1079 TGCCACCTCCCTCAAGGAGTGATATGGACATGTCAGAGTTCTCATTTGGCCAGAGATGT 1138

Qy 1087 CCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA 1146
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Db 1139 TCATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCTCGGAGTGACCTCCTGGCTCA 1198

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Db 1199 CCCCAGCATCCGTCTTTTGTCACTCATGGTGGGCAGAACAGCGTAATGGAGGCCATCCG 1258

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Db 1259 TCATGGTGTGCCCATGGTGGGATTACAGTCAATGGAGACCAGCATGGAAACATGGTCCG 1318

Qy 1267 AGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATT 1326
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Db 1319 AGTAGTAGCCAAAAATTATGGTGTCTCTATCCGGTTGAATCAGGTCACAGCCGACACACT 1378

Qy 1327 GGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGC 1386
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Db 1379 GACACTTACAATGAAACAAGTCATAGAAGACAAGAGGTACAAGTCGGCAGTGGTGGCAGC 1438

Qy 1387 CAGTGTCACTCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGA 1446
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Db 1439 CAGTGTCACTCTGCACTCTCAGCCCCGAGCCCCGACAGCGGCTGGTGGGCTGGATCGA 1498

Qy 1447 CCACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTG 1506
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Db 1499 CCACATCCTCCAGACTGGGGGAGCGACGCACCTCAAGCCCTATGCCTTCCAGCAGCCCTG 1558

Qy 1507 GCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCT 1566
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Db 1559 GCATGAGCAGTACCTCATTGATGTCTTTGTGTTTCTGCTGGGGCTCACTCTGGGCACTAT 1618

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 Qy 1627 GAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGG 1662
 |||| ||||| |||| ||||| ||||| | |
 Db 1679 GAAGAAGACATGAGGCTAGGTGTAGCCTTGGGTGAG 1714

RESULT 14

AX359923

LOCUS AX359923 1572 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 3 from Patent WO0202774.

ACCESSION AX359923

VERSION AX359923.1 GI:18675565

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Leiby, K.R., Cook, W.J. and Spaltmann, F.

TITLE 32626, a human udp-glycosyltransferase and uses thereof

JOURNAL Patent: WO 0202774-A 3 10-JAN-2002;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES

Location/Qualifiers

source

1. .1572

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 52.2%; Score 1212; DB 6; Length 1572;

Best Local Similarity 85.7%; Pred. No. 1.8e-310;

Matches 1347; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

Qy 68 ATGGCTGGGCAGCGAGTGTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTCTCA 127
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 Db 1 ATGGTTGGGCAGCGGGTGTCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCCTGCTCTCA 60
 Qy 128 GAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGAC 187
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 Db 61 GAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGAC 120
 Qy 188 CGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTACCATGCTTAACCACAAAAGA 247
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 Db 121 CGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGGA 180
 Qy 248 GGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTT 307
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| Db | 361 | TGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCTTTAAAGAATGAGAACTATGAT | 420 |
| Qy | 488 | ATGGTGATAGTTGAAACTTTTGGCTACTGTCCTTTCTTGATTGCTGAGAAGCTTGGGAAG | 547 |
| Db | 421 | CTGGTATTTGTTGAAGCATTTGATTTCTGTTCTTTCTTGATTGCTGAGAAGCTTGTGAAA | 480 |
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| Db | 481 | CCATTTGTGGCCATTCTTTCCACCACATTCGGCTCTTTGGAATTTGGGCTACCAAGCCCC | 540 |
| Qy | 608 | TTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGA | 667 |
| Db | 541 | TTGTCTTATGTTCCAGTATTCCCTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGA | 600 |
| Qy | 668 | GTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACA | 727 |
| Db | 601 | GTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTACA | 660 |
| Qy | 728 | TTTGACAACACCATCAAGGAACATTCACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTT | 787 |
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| Qy | 848 | CTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCA | 907 |
| Db | 781 | CTGCTTCCCAACACTGTTTATATTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCA | 840 |
| Qy | 908 | CAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTTG | 967 |
| Db | 841 | CAAGACTTGGAGAACTTCATTGCCAATTTGGGGATGCAGGGTTTGTCTTGTGGCCTTT | 900 |
| Qy | 968 | GGCTCCATGGTGAACACCTGTCAGAATCCGAAATCTTCAAGGAGATGAACAATGCCTTT | 1027 |
| Db | 901 | GGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCTTCAAGAAGATGCACAATGCCTTT | 960 |
| Qy | 1028 | GCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAAGATGTC | 1087 |
| Db | 961 | GCCACCTCCCTCAAGGAGTGATATGGACATGTCAGAGTTCTCATTGGCCCCAGAGATGTT | 1020 |
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Qy      1508 CATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA 1567
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Qy      1568 TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG 1627
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Db      1561 AAGAAGACATGA 1572

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RESULT 15

AR541778

LOCUS AR541778 2426 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 26 from patent US 6743619.

ACCESSION AR541778

VERSION AR541778.1 GI:53933858

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2426)

AUTHORS Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F.,
Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,J.-R.,
Wang,D. and Drmanac,R.T.

TITLE Nucleic acids and polypeptides

JOURNAL Patent: US 6743619-A 26 01-JUN-2004;

FEATURES Location/Qualifiers

source 1. .2426

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 49.5%; Score 1147.8; DB 6; Length 2426;

Best Local Similarity 85.2%; Pred. No. 2.2e-293;

Matches 1281; Conservative 0; Mismatches 222; Indels 0; Gaps 0;

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| Qy | 160 | AGGTGGAAGCCATTATCTACTGATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCA | 219 |
| Db | 617 | AGGTGGAAGCCATTACCTACTGTTGGACCGGGTGTCTCAGATTCTTCAAGAGCATGGTCA | 676 |
| Qy | 220 | TAATGTCACCATGCTTAACCACAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGA | 279 |
| Db | 677 | TAATGTGACTATGCTTCATCAGAGTGGAAAGTTTTTGATCCCAGATATTAAAGAGGAGGA | 736 |
| Qy | 280 | AAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAA | 339 |
| Db | 737 | AAAATCATACCAAGTTATCAGGTGGTTTTTCACCTGAAGATCATCAAAAAGAATTAAGAA | 796 |
| Qy | 340 | GAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATT | 399 |
| Db | 797 | GCATTTTGATAGCTACATAGAAACAGCATTGGATGGCAGAAAAGAATCTGAAGCCCTTGT | 856 |
| Qy | 400 | AAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCAT | 459 |
| Db | 857 | AAAGCTAATGGAAATATTTGGGACTCAATGTAGTTATTTGCTAAGCAGAAAGGATATAAT | 916 |
| Qy | 460 | GGATTCTTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCC | 519 |
| Db | 917 | GGATTCTTTAAAGAATGAGAACTATGATCTGGTATTTGTTGAAGCATTTGATTTCTGTTC | 976 |
| Qy | 520 | TTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGG | 579 |
| Db | 977 | TTTCCTGATTGCTGAGAAGCTTGTGAAACCATTTGTGGCCATTCTTCCCACCACATTCGG | 1036 |
| Qy | 580 | CTCTTTTGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCT | 639 |
| Db | 1037 | CTCTTTTGAATTTGGGCTACCAAGCCCCTTGTCTTATGTTCCAGTATTCCCTTCCCTTGCT | 1096 |
| Qy | 640 | GACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTG | 699 |
| Db | 1097 | GACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTC | 1156 |
| Qy | 700 | CAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTCCACAGA | 759 |
| Db | 1157 | CAGGAGCCAATGGGACATGCAGTCTACATTTGACAACACCATCAAGGAGCATTTCCCAGA | 1216 |
| Qy | 760 | AGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTC | 819 |
| Db | 1217 | AGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTTGTTAACTC | 1276 |
| Qy | 820 | TGACTTTGCCTTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTT | 879 |
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| Qy | 880 | GATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGG | 939 |
| Db | 1337 | GATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGACAACCTTCATTGCCAAGTTTGG | 1396 |
| Qy | 940 | GGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGA | 999 |
| Db | 1397 | GGATGCAGGGTTTTGTCTTGTGGCCTTTGGCTCCATGTTGAACACCCATCAGTCCCAGGA | 1456 |

GenCore version 5.1.6

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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| DE | Human | PRO1780 | nucleotide | sequence | SEQ ID NO:12. | |
| PN | WO200053750-A1. | | | | | |
| PD | 14-SEP-2000. | | | | | |
| PA | (GETH) | GENENTECH | INC. | | | |
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| | Best Local Similarity | 100.0%; | Pred. No. 0; | | | |
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| | Best Local Similarity | 100.0%; | Pred. No. 0; | | | |
| RESULT 3 | | | | | | |
| ID | AAF54401 | standard; | dna; | 2320 | BP. | |
| DE | Primer #82 | used in the | identification | of | proteins. | |
| PN | WO200078961-A1. | | | | | |
| PD | 28-DEC-2000. | | | | | |
| PA | (GETH) | GENENTECH | INC. | | | |

Query Match 100.0%; Score 2320; DB 4; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 4

ID ACD68440 standard; cDNA; 2320 BP.
 DE Novel human secreted and transmembrane protein PRO1780 cDNA.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 5

ID ACH04542 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 6

ID ACD68086 standard; cDNA; 2320 BP.
 DE Novel human secreted and transmembrane protein PRO1780 cDNA.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 7

ID ADC18150 standard; cDNA; 2320 BP.
 DE Human PRO polynucleotide #80.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 8

ID ADD70796 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

ID ADD39873 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 10

ID ADD70319 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 11

ID ADD38440 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003096955-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 12

ID ADD39396 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003096954-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 13

ID ADD38919 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003092061-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 14

ID ADD40350 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 15

ID ADE50571 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003069179-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 16

ID ADE20183 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003092883-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 17

ID ADE50094 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003082626-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 18

ID ADE21652 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 19

ID ADF30077 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 20

ID ADF55970 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 21

ID ADH99474 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 22

ID ADE96654 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 23

ID ADF25965 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 24

ID ADF24864 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 25

ID ADF29600 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 26
 ID ADE97131 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 27
 ID ADH03169 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 28
 ID ADH04123 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 29
 ID ADH03646 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 30
 ID ADH04600 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 31
 ID ADH61601 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 32
 ID ADL94800 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 33
 ID AAF93775 standard; cDNA; 2341 BP.
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0073.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 99.6%; Score 2310.2; DB 5; Length 2341;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 34
 ID AAL41485 standard; DNA; 2944 BP.
 DE Drug metabolising enzyme encoding DNA - 7486594CB1.
 PN WO200266654-A2.
 PD 29-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 90.6%; Score 2102.8; DB 6; Length 2944;
 Best Local Similarity 95.5%; Pred. No. 0;
 RESULT 35
 ID AAS62475 standard; cDNA; 2074 BP.
 DE cDNA sequence #262 encoding novel human secreted protein.
 PN WO200177291-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 88.9%; Score 2063.4; DB 6; Length 2074;
 Best Local Similarity 99.7%; Pred. No. 0;
 RESULT 36
 ID ADR19692 standard; DNA; 2263 BP.
 DE Human drug metabolising enzyme (DME)-13 gene sequence.
 PN WO200226988-A2.
 PD 04-APR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 68.1%; Score 1578.8; DB 7; Length 2263;
 Best Local Similarity 92.6%; Pred. No. 0;
 RESULT 37
 ID AAD06821 standard; cDNA; 2797 BP.
 DE Human secreted protein Zalpa37 cDNA.
 PN WO200138505-A2.
 PD 31-MAY-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 55.2%; Score 1281.6; DB 4; Length 2797;
 Best Local Similarity 85.9%; Pred. No. 0;
 RESULT 38
 ID ADA53720 standard; cDNA; 2823 BP.
 DE Human coding sequence, SEQ ID 1288.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 55.2%; Score 1281.6; DB 10; Length 2823;
 Best Local Similarity 85.9%; Pred. No. 0;
 RESULT 39
 ID AAD24667 standard; cDNA; 2086 BP.

DE Human drug metabolising enzyme (DME)-2 cDNA.

PN WO200179468-A2.

PD 25-OCT-2001.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 55.2%; Score 1280; DB 6; Length 2086;

Best Local Similarity 85.8%; Pred. No. 0;

RESULT 40

ID ABK90831 standard; cDNA; 1851 BP.

DE cDNA encoding drug metabolising enzyme.

PN US2002082194-A1.

PD 27-JUN-2002.

PA (GUEG/) GUEGLER K.

PA (WEBS/) WEBSTER M.

PA (YANC/) YAN C.

PA (DFRA/) DI FRANCESCO V.

PA (BEAS/) BEASLEY E M.

Query Match 54.8%; Score 1270.4; DB 6; Length 1851;

Best Local Similarity 85.9%; Pred. No. 0;

RESULT 41

ID ADN02571 standard; DNA; 2868 BP.

DE Human hepatouracil dinucleotide glycosyltransferase 29.7 DNA.

PN CN1393551-A.

PD 29-JAN-2003.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

Query Match 54.5%; Score 1264.8; DB 11; Length 2868;

Best Local Similarity 85.6%; Pred. No. 0;

RESULT 42

ID AAD25345 standard; cDNA; 2082 BP.

DE Human UDP-glycosyltransferase, 32626 cDNA.

PN WO200202774-A2.

PD 10-JAN-2002.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 54.2%; Score 1257.6; DB 6; Length 2082;

Best Local Similarity 85.0%; Pred. No. 0;

RESULT 43

ID ABL57726 standard; DNA; 1572 BP.

DE Human sbg100540UDPGT gene #2.

PN WO200222802-A1.

PD 21-MAR-2002.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PA (GLAX) GLAXO GROUP LTD.

Query Match 52.2%; Score 1212; DB 6; Length 1572;

Best Local Similarity 85.7%; Pred. No. 0;

RESULT 44

ID ADA21188 standard; cDNA; 2268 BP.

DE Human secreted protein SECP-42 encoding cDNA SEQ ID NO:93.

PN WO2003068943-A2.

PD 21-AUG-2003.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 49.5%; Score 1147.8; DB 9; Length 2268;

Best Local Similarity 85.2%; Pred. No. 0;

RESULT 45

ID ABX70800 standard; cDNA; 2426 BP.

DE Novel human cDNA sequence #25.

PN WO200281731-A2.

PD 17-OCT-2002.

PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match 49.5%; Score 1147.8; DB 8; Length 2426;
Best Local Similarity 85.2%; Pred. No. 0;
RESULT 46
ID ADQ75567 standard; cDNA; 2791 BP.
DE Uridine diphosphate-galactosyl ceramide glucuronyl collagen transferase.
PN CN1380409-A.
PD 20-NOV-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 49.5%; Score 1147.8; DB 11; Length 2791;
Best Local Similarity 85.2%; Pred. No. 0;
RESULT 47
ID ABL57725 standard; DNA; 1182 BP.
DE Human sbg10054OUDPGT gene #1.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 41.2%; Score 956.4; DB 6; Length 1182;
Best Local Similarity 88.1%; Pred. No. 4.4e-274;
RESULT 48
ID AAD06822 standard; DNA; 1569 BP.
DE Human secreted protein Zalpa37 degenerate coding sequence.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 40.7%; Score 944.8; DB 4; Length 1569;
Best Local Similarity 52.4%; Pred. No. 1.5e-270;
RESULT 49
ID AAD06823 standard; cDNA; 2212 BP.
DE Mouse secreted protein Zalpa37 cDNA.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 39.3%; Score 910.8; DB 4; Length 2212;
Best Local Similarity 73.0%; Pred. No. 2.8e-260;
RESULT 50
ID AAS84832 standard; cDNA; 2721 BP.
DE DNA encoding novel human diagnostic protein #20636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 34.9%; Score 808.8; DB 5; Length 2721;
Best Local Similarity 95.8%; Pred. No. 9.2e-230;
RESULT 51
ID AAD06824 standard; DNA; 1569 BP.
DE Mouse secreted protein Zalpa37 degenerate coding sequence.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 34.0%; Score 789; DB 4; Length 1569;
Best Local Similarity 47.8%; Pred. No. 5.2e-224;
RESULT 52
ID ABA09537 standard; cDNA; 1898 BP.
DE Human PRO1780 homologue-encoding cDNA, SEQ ID NO:1313.

PN WO200157188-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 30.5%; Score 708.2; DB 4; Length 1898;
 Best Local Similarity 86.4%; Pred. No. 8e-200;
 RESULT 53
 ID AAF93971 standard; DNA; 770 BP.
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 405.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 25.7%; Score 595.2; DB 5; Length 770;
 Best Local Similarity 93.4%; Pred. No. 2.4e-166;
 RESULT 54
 ID ADB62657 standard; cDNA; 1842 BP.
 DE Human cDNA encoding clone KIDNE20186170.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 25.6%; Score 593.4; DB 10; Length 1842;
 Best Local Similarity 85.6%; Pred. No. 1.5e-165;
 RESULT 55
 ID ADQ64368 standard; cDNA; 5002 BP.
 DE Novel human cDNA sequence #1529.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 24.8%; Score 575.4; DB 12; Length 5002;
 Best Local Similarity 85.3%; Pred. No. 6.9e-160;
 RESULT 56
 ID AAF94120 standard; DNA; 594 BP.
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 554.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 23.2%; Score 538.4; DB 5; Length 594;
 Best Local Similarity 98.5%; Pred. No. 1.9e-149;
 RESULT 57
 ID AAS81804 standard; cDNA; 2220 BP.
 DE DNA encoding novel human diagnostic protein #17608.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.0%; Score 487.6; DB 5; Length 2220;
 Best Local Similarity 93.7%; Pred. No. 6.7e-134;
 RESULT 58
 ID ADN39359 standard; cDNA; 923 BP.
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B43.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 19.0%; Score 441; DB 11; Length 923;
 Best Local Similarity 100.0%; Pred. No. 3.1e-120;
 RESULT 59
 ID ABK90832 standard; DNA; 42999 BP.
 DE Genomic DNA encoding drug metabolising enzyme.

PN US2002082194-A1.
 PD 27-JUN-2002.
 PA (GUEG/) GUEGLER K.
 PA (WEBS/) WEBSTER M.
 PA (YANC/) YAN C.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 18.7%; Score 433.6; DB 6; Length 42999;
 Best Local Similarity 88.1%; Pred. No. 6.4e-117;
 RESULT 60
 ID AAS81803 standard; cDNA; 659 BP.
 DE DNA encoding novel human diagnostic protein #17607.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 17.2%; Score 399.6; DB 5; Length 659;
 Best Local Similarity 92.5%; Pred. No. 5.7e-108;
 RESULT 61
 ID AAS41046 standard; cDNA; 923 BP.
 DE cDNA encoding novel human enzyme polypeptide #262.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.8%; Score 319.6; DB 4; Length 923;
 Best Local Similarity 84.8%; Pred. No. 5.5e-84;
 RESULT 62
 ID AAS41586 standard; cDNA; 981 BP.
 DE cDNA encoding novel human enzyme polypeptide #802.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.8%; Score 319.4; DB 4; Length 981;
 Best Local Similarity 85.4%; Pred. No. 6.6e-84;
 RESULT 63
 ID AAL01667 standard; cDNA; 981 BP.
 DE Human reproductive system related antigen cDNA SEQ ID NO: 1668.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.8%; Score 319.4; DB 4; Length 981;
 Best Local Similarity 85.4%; Pred. No. 6.6e-84;
 RESULT 64
 ID ADQ57767 standard; DNA; 582 BP.
 DE Novel canine microarray-related DNA sequence SeqID9069.
 PN WO2004063324-A2.
 PD 29-JUL-2004.
 PA (GENE-) GENE LOGIC INC.
 PA (PFIZ) PFIZER PROD INC.
 Query Match 13.6%; Score 314.8; DB 13; Length 582;
 Best Local Similarity 81.8%; Pred. No. 1.1e-82;
 RESULT 65
 ID AAL05664 standard; DNA; 5973 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8352.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.3%; Score 239.2; DB 4; Length 5973;

Best Local Similarity 86.0%; Pred. No. 2e-59;

RESULT 66

ID AAK11854 standard; DNA; 507 BP.

DE Human brain expressed single exon probe SEQ ID NO: 11845.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 10.3%; Score 238.8; DB 4; Length 507;

Best Local Similarity 86.3%; Pred. No. 5e-60;

RESULT 67

ID AAL05663 standard; DNA; 2751 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8351.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 238.8; DB 4; Length 2751;

Best Local Similarity 86.3%; Pred. No. 1.5e-59;

RESULT 68

ID AAL05665 standard; DNA; 5974 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8353.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 238.8; DB 4; Length 5974;

Best Local Similarity 86.3%; Pred. No. 2.6e-59;

RESULT 69

ID AAS84831 standard; cDNA; 1242 BP.

DE DNA encoding novel human diagnostic protein #20635.

PN WO200175067-A2.

PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.

Query Match 9.7%; Score 224; DB 5; Length 1242;

Best Local Similarity 100.0%; Pred. No. 2.4e-55;

RESULT 70

ID AAS82074 standard; cDNA; 1242 BP.

DE DNA encoding novel human diagnostic protein #17878.

PN WO200175067-A2.

PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.

Query Match 9.7%; Score 224; DB 5; Length 1242;

Best Local Similarity 100.0%; Pred. No. 2.4e-55;

RESULT 71

ID AAK24438 standard; DNA; 277 BP.

DE Human brain expressed single exon probe SEQ ID NO: 24429.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 9.5%; Score 220; DB 4; Length 277;

Best Local Similarity 87.3%; Pred. No. 1.4e-54;

RESULT 72

ID ABI99695 standard; cDNA; 2308 BP.

DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:738.

PN WO200188188-A2.

PD 22-NOV-2001.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

Query Match 7.1%; Score 164; DB 6; Length 2308;

Best Local Similarity 47.5%; Pred. No. 3e-37;

RESULT 73

ID ACN45084 standard; DNA; 49753 BP.

DE Mouse genomic sequence mCG7831.

PN WO2003073826-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.

Query Match 7.0%; Score 162.6; DB 11; Length 49753;

Best Local Similarity 72.7%; Pred. No. 6e-36;

RESULT 74

ID ADB59021 standard; DNA; 1716 BP.

DE Toxicity-related gene, SEQ ID 4047.

PN WO2003064624-A2.

PD 07-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 10; Length 1716;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 75

ID ADB53779 standard; DNA; 1716 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4321.

PN WO2003065993-A2.

PD 14-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 10; Length 1716;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 76

ID ADP73008 standard; DNA; 1716 BP.

DE Renal toxin progression gene marker #1597.

PN WO2004048598-A2.

PD 10-JUN-2004.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 12; Length 1716;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 77

ID ADP72663 standard; DNA; 1819 BP.

DE Renal toxin progression gene marker #1252.

PN WO2004048598-A2.

PD 10-JUN-2004.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 12; Length 1819;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 78

ID ABK63496 standard; cDNA; 1961 BP.

DE Rat sequence differentially expressed in response to a hepatotoxin #1403.

PN WO200210453-A2.

PD 07-FEB-2002.

PA (GENE-) GENE LOGIC INC.

Query Match 6.3%; Score 145.2; DB 6; Length 1961;

Best Local Similarity 49.4%; Pred. No. 1.1e-31;

RESULT 79

ID ADB57963 standard; DNA; 1961 BP.

DE Toxicity-related gene, SEQ ID 2989.

PN WO2003064624-A2.

PD 07-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Query Match 6.3%; Score 145.2; DB 10; Length 1961;

Best Local Similarity 49.4%; Pred. No. 1.1e-31;

RESULT 80

ID ABZ58827 standard; cDNA; 1584 BP.
 DE Human 32624 polypeptide coding sequence.
 PN WO200226834-A2.
 PD 04-APR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 6.2%; Score 144.2; DB 6; Length 1584;
 Best Local Similarity 48.4%; Pred. No. 1.9e-31;
 RESULT 81
 ID ABZ58826 standard; cDNA; 2996 BP.
 DE Human 32624 polypeptide encoding cDNA.
 PN WO200226834-A2.
 PD 04-APR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 6.2%; Score 144.2; DB 6; Length 2996;
 Best Local Similarity 48.4%; Pred. No. 2.9e-31;
 RESULT 82
 ID AAD24666 standard; cDNA; 1636 BP.
 DE Human drug metabolising enzyme (DME)-1 cDNA.
 PN WO200179468-A2.
 PD 25-OCT-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 6.2%; Score 143.2; DB 6; Length 1636;
 Best Local Similarity 48.3%; Pred. No. 3.9e-31;
 RESULT 83
 ID ADA11047 standard; cDNA; 1636 BP.
 DE Human cDNA differentially expressed in colon cancer #117.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 6.2%; Score 143.2; DB 9; Length 1636;
 Best Local Similarity 48.3%; Pred. No. 3.9e-31;
 RESULT 84
 ID ADS09871 standard; DNA; 2408 BP.
 DE Human therapeutic DNA - SEQ ID 108.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 6.2%; Score 143.2; DB 13; Length 2408;
 Best Local Similarity 48.3%; Pred. No. 5e-31;
 RESULT 85
 ID ABK12422 standard; cDNA; 2759 BP.
 DE cDNA encoding human drug-metabolising enzyme.
 PN WO200218554-A2.
 PD 07-MAR-2002.
 PA (APPL-) APPLERA CORP.
 Query Match 6.2%; Score 143.2; DB 6; Length 2759;
 Best Local Similarity 48.3%; Pred. No. 5.5e-31;
 RESULT 86
 ID ADA10915 standard; cDNA; 2966 BP.
 DE Human cDNA differentially expressed in colon cancer #22.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 6.2%; Score 143.2; DB 9; Length 2966;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 87

ID ADL12512 standard; cDNA; 2966 BP.
DE Human steroid-induced C3A liver cell cDNA #241.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 143.2; DB 12; Length 2966;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 88

ID AAS46185 standard; cDNA; 2974 BP.
DE Human DNA encoding PRO polypeptide sequence #261.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 4; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 89

ID ACA89635 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 90

ID ACA73645 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 91

ID ACA05960 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 92

ID ACA66794 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO protein #261.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 93

ID ACF20369 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 94

ID ACF19755 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040064-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 95

ID ACD22043 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003027267-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 96

ID ACF13208 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036160-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 97

ID ACD25311 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044925-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 98

ID ACF00360 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003054474-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 99

ID ACA72417 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032114-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 100

ID ACD04941 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032101-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 101

ID ACD18402 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036124-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 102

ID ACD08409 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003040054-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 103

ID ACA88843 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036133-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 104

ID ACA70285 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036134-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 105

ID ACD12507 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003022294-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 106

ID ACC74422 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027275-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 107

ID ACD16050 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003027324-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 108

ID ACD25618 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036118-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 109

ID ACD18095 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036123-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 110

ID ACC88382 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036148-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 111

ID ACD21736 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003040060-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 112

ID ACD18803 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044916-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 113

ID ABX98413 standard; cDNA; 2974 BP.

DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 521.

PN US2003036156-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 114

ID ACD14164 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032117-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 115

ID ACD09944 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036128-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 116

ID ACC88689 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027266-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 117

ID ACD21429 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003054483-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 118

ID ABX75801 standard; cDNA; 2974 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO6239.

PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 119
ID ABX98004 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 120
ID ACA97480 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 121
ID ACA57943 standard; cDNA; 2974 BP.
DE Human PRO6239 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 122
ID ACD14471 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 123
ID ACC91254 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 124
ID ACC88996 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 125
ID ACD07193 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 126
ID ACA67644 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 127
ID ACC81699 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 128
ID ACC89303 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 129
ID ACC86659 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 130
ID ACC89917 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 131
ID ACC93096 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 132
ID ACA72724 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 133
ID ACA89242 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 134
ID ACA69978 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 135
ID ACA97121 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 136
ID ACA91117 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 137
ID ACA70899 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 138
ID ACA95409 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 139
ID ACC86352 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 140
ID ACC90224 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 141
ID ACD12832 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 142
ID ACF20062 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040068-A1.
PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 143

ID ABX77006 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003027280-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 144

ID ACA73338 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003022300-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 145

ID ACA68881 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036136-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 146

ID ACA74725 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003036138-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 147

ID ACA70592 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032109-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 148

ID ACD14778 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003040066-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 149

ID ACA68450 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032104-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 150

ID ABX98915 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036157-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 151

ID ACC81392 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032120-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 152

ID ACA95716 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036155-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 153

ID ACD04634 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003022296-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 154

ID ACC88075 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027281-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 155

ID ACF12737 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040058-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 156

ID ACA96452 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003017540-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 157

ID ACA65226 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032106-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 158

ID ACA73952 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032129-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 159

ID ACA74364 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032131-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 160

ID ACA96759 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032103-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 161

ID ACD10865 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003032107-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 162

ID ACC91561 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032139-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 163

ID ACD02896 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003022301-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 164

ID ACC87461 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036165-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 165

ID ACC86045 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027262-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 166

ID ACA65533 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032110-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 167

ID ACA94350 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036142-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 168

ID ACA98094 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003036145-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 169

ID ACA91596 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036154-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 170

ID ACA90810 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036153-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 171

ID ACD16357 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044931-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 172

ID ACD17518 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036150-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 173

ID ACC92175 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040069-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 174

ID ACA75032 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003022293-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 175

ID ACA91903 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032128-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 176

ID ACA71547 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032116-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 177

ID ACC90947 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032122-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 178

ID ACA65957 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO protein #261.

PN US2003036139-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 179

ID ACA95102 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003017541-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 180

ID ACD16664 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003017543-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 181

ID ACD15743 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036152-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 182

ID ABX16846 standard; cDNA; 2974 BP.

DE Human cDNA encoding secreted/transmembrane protein #261.

PN US2002127584-A1.

PD 12-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 183

ID ACA97787 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032115-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 184

ID ACA99236 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032140-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 185

ID ACC91868 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040076-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 186

ID ACD11279 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003008352-A1.

PD 09-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 187

ID ACD15129 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044922-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 188

ID ACD11893 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032118-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 189

ID ACC96022 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036135-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 190

ID ACF16585 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003054455-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 191
 ID ACF02703 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049741-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 192
 ID ACF03010 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 193
 ID ACF21597 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 194
 ID ACF10281 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068743-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 195
 ID ACF78174 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054479-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 196
 ID ACD46879 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068685-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 197
 ID ACD49642 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068725-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 198
ID ACF28409 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 199
ID ACD89099 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 200
ID ACD84494 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 201
ID ACD99268 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 202
ID ADA78273 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 203
ID ACF49010 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 204
ID ACD09330 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 205
 ID ACF12123 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040075-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 206
 ID ACF41357 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054459-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 207
 ID ACF15971 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044930-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 208
 ID ACF16278 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040071-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 209
 ID ACD32105 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054471-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 210
 ID ACF18913 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064452-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 211
 ID ACF09360 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068705-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 212
 ID ACF78481 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 213

ID ACF52080 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064440-A1.
PD 03-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 214

ID ACF26567 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 215

ID ACF24360 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 216

ID ACF63671 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 217

ID ACF50545 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 218

ID ACH08016 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 219

ID ACF13822 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064462-A1.

PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 220
 ID ACD41748 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003065159-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 221
 ID ACF32161 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064447-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 222
 ID ACF23439 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073184-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 223
 ID ACF40129 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064463-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 224
 ID ACD45651 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261..
 PN US2003064451-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 225
 ID ACF53308 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 226
 ID ACF27488 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068699-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 227
 ID ACF45326 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068707-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 228
 ID ACF29944 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 229
 ID ACD90020 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 230
 ID ACD84801 standard; cDNA; 2974 BP.
 DE Human PRO polynucleotide #261.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 231
 ID ACD98961 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 232
 ID ACF77253 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521....
 PN US2003082717-A1.
 PD 01-MAY-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 233
 ID ACF76946 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 234
 ID ACF49931 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 235
 ID ACF50238 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 236
 ID ACD09637 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003036127-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 237
 ID ACD08716 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003040061-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 238
 ID ACF12430 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003036130-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 239
 ID ACC94938 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 240
 ID ACD22657 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054470-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 241
 ID ACF15357 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044917-A1.
 PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 242
 ID ACC97452 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044929-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 243
 ID ACC92482 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003059880-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 244
 ID ACF14129 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 245
 ID ACF14436 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 246
 ID ACF09667 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068718-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 247
 ID ACD45958 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 248
 ID ACD48107 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 249

ID ACD67838 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 250

ID ACF25646 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 251

ID ACF29330 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 252

ID ACD85108 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 253

ID ACD84187 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 254

ID ACD88178 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 255

ID ACF30865 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 256

ID ACF32468 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104555-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 257
 ID ACH12128 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 258
 ID ACH12435 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 259
 ID ACD40827 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 260
 ID ACF18299 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054481-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 261
 ID ACF08746 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049778-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 262
 ID ACF31547 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049782-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 263
 ID ACF52387 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003054476-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 264
 ID ACD50256 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068733-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 265
 ID ACF38959 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068692-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 266
 ID ACF26874 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068709-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 267
 ID ACF24974 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068716-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 268
 ID ACF46554 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068740-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 269
 ID ACF28102 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068751-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 270
 ID ACD89406 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068684-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 271
 ID ACF63978 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073179-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 272
 ID ACF60618 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003087374-A1.
 PD 08-MAY-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 273
 ID ACH12742 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049773-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 274
 ID ACH10165 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049777-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 275
 ID ACD04020 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003040055-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 276
 ID ACD10558 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003036164-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 277
 ID ACF42585 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054480-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 278

ID ACF18606 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 279

ID ACF02396 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 280

ID ACF21904 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 281

ID ACF10588 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073169-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 282

ID ACF34040 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 283

ID ACF45002 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 284

ID ACD90634 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 285

ID ACD91247 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 286
ID ACF30558 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 287
ID ACD87257 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 288
ID ACF60311 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 289
ID ACF46861 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 290
ID ACF75718 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 291
ID ADA80065 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 292
ID ACF17378 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 293
 ID ACF23132 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003059886-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 294
 ID ACF08132 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049758-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 295
 ID ACF08439 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049772-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 296
 ID ACF40743 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064448-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 297
 ID ACF53922 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064456-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 298
 ID ACD47186 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068693-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 299
 ID ACF48089 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068735-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 300

ID ACF47475 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 301

ID ACF46247 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 302

ID ACD86336 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 303

ID ACF52694 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003082715-A1.
PD 01-MAY-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 304

ID ACF53001 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003082716-A1.
PD 01-MAY-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 305

ID ACF64994 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 306

ID ACF76639 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 307

ID ACF61539 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003096359-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 308
 ID ACF61846 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003100061-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 309
 ID ACD30877 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003032125-A1.
 PD 13-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 310
 ID ACD31798 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054454-A1.
 PD 20-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 311
 ID ACD32719 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054477-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 312
 ID ACF17685 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054460-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 313
 ID ACF07518 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049753-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 314
 ID ACF20676 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049763-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 315
 ID ACF21290 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073172-A1.
 PD 17-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 316
 ID ACF20983 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073172-A1.
 PD 17-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 317
 ID ACD47800 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068700-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 318
 ID ACF47782 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068736-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 319
 ID ACF53615 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068679-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 320
 ID ACD86950 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068767-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 321
 ID ACH05198 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003073182-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 322

ID ACF44695 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 323

ID ADA81792 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 324

ID ACD22350 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003027276-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 325

ID ACD24697 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003044920-A1.
PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 326

ID ACD39900 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003027265-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 327

ID ACD40207 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 328

ID ACF13515 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064446-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 329

ID ACF03317 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049744-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 330

ID ACF78788 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003049783-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 331

ID ACF11509 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003073171-A1.

PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 332

ID ACF50852 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032121-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 333

ID ACF34347 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003064458-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 334

ID ACD46572 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003064460-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 335

ID ACD48414 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003064464-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 336

ID ACF27795 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068702-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 337

ID ACF24667 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 338

ID ACD85722 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 339

ID ACD90327 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 340

ID ACD83880 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 341

ID ACF49317 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104540-A1.
PD 05-JUN-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 342

ID ACH07402 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 343

ID ACH07709 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 344

ID ACH08323 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 345

ID ACH11514 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 346

ID ACH11821 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 347

ID ACH10472 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 348

ID ACF01475 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040059-A1.
PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 349

ID ACF41050 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 350

ID ACD24390 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003044918-A1.
PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 351

ID ACD31491 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032132-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 352
 ID ACF17992 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054462-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 353
 ID ACF32775 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064445-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 354
 ID ACF40436 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064449-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 355
 ID ACF48396 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064441-A1.
 PD 03-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 356
 ID ACF38345 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068696-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 357
 ID ACF25281 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068712-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 358
 ID ACF27181 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068730-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 359

ID ACF29637 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073174-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 360

ID ACD87871 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 361

ID ACF76332 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 362

ID ACF49624 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104541-A1.
PD 05-JUN-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 363

ID ACF44081 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 364

ID ACH06426 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 365

ID ACH06733 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 366

ID ADA83590 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003049752-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 367
 ID ACC92789 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003032133-A1.
 PD 13-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 368
 ID ACC93403 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003032136-A1.
 PD 13-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 369
 ID ACF19448 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003036129-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 370
 ID ACD13139 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003040053-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 371
 ID ACF06597 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040057-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 372
 ID ACC94631 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054467-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 373
 ID ACC98059 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044932-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 374
 ID ACC94324 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027270-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 375

ID ACF42278 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 376

ID ACD31184 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032126-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 377

ID ACD43213 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 378

ID ACD43520 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 379

ID ACF15050 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 380

ID ACF01782 standard; cDNA; 2974 BP..
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049738-A1.
PD 13-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 381

ID ACF31854 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 382
 ID ACD67531 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003064453-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 383
 ID ACD48721 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064466-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 384
 ID ACD49028 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064468-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 385
 ID ACF51466 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068760-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 386
 ID ACF54229 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068769-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 387
 ID ACF25953 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 388
 ID ACF39266 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068698-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 389
 ID ACF29023 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068759-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 390
 ID ACD90940 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049748-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 391
 ID ACD86643 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068765-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 392
 ID ACH05505 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049754-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 393
 ID ACF65301 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068688-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 394
 ID ADB20633 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003082767-A1.
 PD 01-MAY-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 395
 ID ACF43774 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104552-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 396

ID ACH09244 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049774-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 397
 ID ACH09551 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 398
 ID ADA78885 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 399
 ID ACF09974 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068720-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 400
 ID ACF51159 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068739-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 401
 ID ACF24053 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068763-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 402
 ID ACD88485 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068689-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 403
 ID ACH09858 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049776-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 404
 ID ACH10779 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049780-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 405
 ID ACD11586 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003036126-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 406
 ID ACC96636 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044924-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 407
 ID ACC98666 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044927-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 408
 ID ACF41971 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040072-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 409
 ID ACF16892 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040073-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 410
 ID ACD32412 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054475-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 411

ID ACD30570 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032124-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 412

ID ACD41441 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 413

ID ACF07825 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 414

ID ACF31240 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 415

ID ACF77560 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 416

ID ACF11202 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073170-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 417

ID ACF33082 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 418

ID ACF26260 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068717-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 419

ID ACD83573 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003068728-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 420

ID ACF23746 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068764-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 421

ID ACF43160 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003104550-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 422

ID ACF43467 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003104551-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 423

ID ACH06119 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003049761-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 424

ID ACH08937 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003049757-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 425

ID ACC90531 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027273-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 426

ID ACF10895 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036119-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 427

ID ACC93710 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036120-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 428

ID ACC96329 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036161-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 429

ID ACD25004 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044921-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 430

ID ACF02089 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003049739-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 431

ID ACF22211 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003059882-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 432

ID ACF22825 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003059884-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 433

ID ACF09053 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068687-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 434
 ID ACF33389 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073186-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 435
 ID ACF54843 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064443-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 436
 ID ACF48703 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064444-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 437
 ID ACD47493 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068697-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 438
 ID ACD49335 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068710-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 439
 ID ACF38038 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068686-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 440
 ID ACF30251 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 441
ID ACD87564 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 442
ID ACF62153 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 443
ID ACH11086 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 444
ID ACD10251 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 445
ID ACD16976 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 446
ID ACC99273 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 447
ID ACF00667 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 448

ID ACD41134 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 449

ID ACF14743 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 450

ID ACF22518 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 451

ID ACF79095 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 452

ID ACF11816 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 453

ID ACF51773 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 454

ID ACF33696 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 455

ID ACD49949 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 456
 ID ACF37731 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068683-A1.
 PD 10-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 457
 ID ACF28716 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068754-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 458
 ID ACD88792 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068681-A1.
 PD 10-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 459
 ID ACF75411 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003096351-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 460
 ID ACF61232 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003096358-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 461
 ID ACF44388 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104556-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 462
 ID ACH08630 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049756-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 463
ID ACC94017 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 464
ID ACD21122 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 465
ID ACF06904 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 466
ID ACD20815 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 467
ID ACD22964 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 468
ID ACF41664 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 469
ID ACF07211 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 470
ID ACF77867 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 471
ID ACD46265 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 472
ID ACF47168 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 473
ID ACF54536 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 474
ID ACF45940 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 475
ID ACF45633 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 476
ID ACF38652 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 477
ID ACD89713 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.